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OM protein - protein search, using sw model

Run on: October 22, 2001, 16:03:50 ; Search time 13.88 Seconds
(without alignments)
1192.697 Million cell updates/sec

Title: us-09-116-676-10

Perfect score: 4363

Sequence: 1 MICQKFCVLLHWEFYIVT.....WLRISSVKYYIHGKFTIL 804

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4337	99.4	1165	2	US-08-599-455B-4
2	4325	99.1	898	2	US-08-693-697-36
3	4325	99.1	908	2	US-08-693-697-33
4	4325	99.1	960	1	US-08-355-888A-8
5	4325	99.1	960	2	US-08-693-697-8
6	4325	99.1	960	2	US-08-640-389A-3
7	4325	99.1	960	3	US-08-693-696-8
8	4320	99.0	960	2	US-08-588-190-3
9	4315	98.9	908	2	US-08-588-526-3
10	4309	98.8	1165	2	US-08-640-389A-11
11	4297	98.5	896	2	US-08-640-389A-10
12	4297	98.5	906	2	US-08-640-389A-9
13	4297	98.5	958	2	US-08-640-389A-8
14	4291	98.0	896	2	US-08-640-389A-12
15	3345	76.7	894	2	US-08-599-455B-2
16	3345	76.7	1162	2	US-08-599-455B-43
17	3057	70.1	569	1	US-08-306-231-3
18	277.5	6.4	488	2	US-08-599-455B-5
19	277.5	6.4	658	2	US-08-825-558-4
20	277.5	6.4	708	1	US-07-797-556-2
21	277.5	6.4	708	1	US-08-308-881-2
22	277.5	6.4	708	2	US-09-058-263-2
23	277.5	6.4	708	2	US-09-059-099-2
24	277.5	6.4	708	3	US-09-058-264-2
25	277.5	6.4	708	5	PCT-US95-06530-2
26	277.5	6.4	918	2	US-08-825-558-6
27	246.5	5.6	837	1	US-07-923-976-2

28	242.5	5.6	771	1	US-07-923-976-6
29	242.5	5.6	783	6	5422248-2
30	242.5	5.6	836	1	US-07-923-976-4
31	242.5	5.6	863	1	US-07-923-976-8
32	221.5	5.1	1001	1	US-07-797-556-6
33	221.5	5.1	1001	1	US-07-943-843-2
34	221.5	5.1	1001	1	US-08-347-003-2
35	221.5	5.1	1097	1	US-07-943-843-6
36	221.5	5.1	1097	1	US-08-347-003-6
37	212.5	4.9	979	1	US-08-308-881-6
38	212.5	4.9	979	2	US-09-058-263-6
39	212.5	4.9	979	2	US-09-059-099-6
40	212.5	4.9	979	3	US-09-058-264-6
41	212.5	4.9	979	5	PCT-US95-06530-6
42	211	4.8	602	2	US-08-419-652-6
43	208	4.8	719	1	US-07-943-843-4
44	208	4.8	719	1	US-08-347-003-4
45	200.5	4.6	862	2	US-08-685-118-2

ALIGNMENTS

RESULT 1
US-08-599-455B-4
; Sequence 4, Application US/08599455B
; Patent No. 5972621
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Tepper, Robert I.
; TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
; TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,455B
; FILING DATE: 22-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/583,153
; FILING DATE: 28-DEC-1995
; APPLICATION NUMBER: 08/570,142
; FILING DATE: 11-DEC-1995
; APPLICATION NUMBER: 08/569,485
; FILING DATE: 08-DEC-1995
; APPLICATION NUMBER: 08/566,622
; FILING DATE: 04-DEC-1995
; APPLICATION NUMBER: 08/562,663
; FILING DATE: 27-NOV-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown

MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-599-455B-4

Query Match 99.4%; Score 4337; DB 2; Length 1165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPTTPWRFKLSQMPNPNSTYDYFLLPAGLSKNTSNS 60
DB 1 MICQKFCVLLHWEFIYVITAFNLSYPTTPWRFKLSQMPNPNSTYDYFLLPAGLSKNTSNS 60

QY 61 NGHYETAPEPKFNSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 120
DB 61 NGHYETAPEPKFNSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 120

QY 121 QIDANNIOCWLGDKLKFICYVESLFKNLFNRYNFKVHLLVYLPVLEDSPLVPQKGS 180
DB 121 QIDANNIOCWLGDKLKFICYVESLFKNLFNRYNFKVHLLVYLPVLEDSPLVPQKGS 180

QY 181 FQVHCNCSVHECCVLPVPTAKLNDTLMLCKITSGVIFQSPPLMSVQPINMKVDPDP 240
DB 181 FQVHCNCSVHECCVLPVPTAKLNDTLMLCKITSGVIFQSPPLMSVQPINMKVDPDP 240

QY 241 LGLHMEITDDGNLKSWSPPPLVPPLOQYQVYKYSNSTTVIREADKIVSATSLLVDSILP 300
DB 241 LGLHMEITDDGNLKSWSPPPLVPPLOQYQVYKYSNSTTVIREADKIVSATSLLVDSILP 300

QY 301 GSSYEVOVRKRLDGGPGIWSDNSTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKNKI 360
DB 301 GSSYEVOVRKRLDGGPGIWSDNSTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKNKI 360

QY 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFNFKNETKPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFNFKNETKPRGKFTYDAVYCCNEHECHH 420

QY 421 RYAEIYVIVDWININISCTDGYLTMTKCRNSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480
DB 421 RYAEIYVIVDWININISCTDGYLTMTKCRNSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480

QY 481 PISEPKDCYLOSGDGYECIFQPIFLLSGYTMMIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYLOSGDGYECIFQPIFLLSGYTMMIRINHSLSGSDSPPTCVLPDSVVKPLPP 540

QY 541 SSVKAEITINICLLKISWEKVPFPENNIFQIRYGLSGKEVQWKMVEYDYDAKSVSPLV 600
DB 541 SSVKAEITINICLLKISWEKVPFPENNIFQIRYGLSGKEVQWKMVEYDYDAKSVSPLV 600

QY 601 PDLCAVAVQVRCRDLGLGYWNSNPAYTVVMDIKVPMRGPEFWRIIDGTHKKKNV 660
DB 601 PDLCAVAVQVRCRDLGLGYWNSNPAYTVVMDIKVPMRGPEFWRIIDGTHKKKNV 660

QY 661 TLLMKPLKNDLSQVRYVNHHTSCNGTWSVDGNHTKFTFLWTEQAHVTVLAINSI 720
DB 661 TLLMKPLKNDLSQVRYVNHHTSCNGTWSVDGNHTKFTFLWTEQAHVTVLAINSI 720

QY 721 GASVANFNLTFSWPKSKYNIQSLAYSAYPLNSSCVIVSWILSPSYDKLMYFTIEWKNLNE 780
DB 721 GASVANFNLTFSWPKSKYNIQSLAYSAYPLNSSCVIVSWILSPSYDKLMYFTIEWKNLNE 780

QY 781 GEIKWLRISSSVKVKYIHGKF 801
DB 781 GEIKWLRISSSVKVKYIHDHF 801

RESULT 2

US-08-693-697-36
Sequence 36, Application US/08693697
Patent No. 5869610
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Cioffi, Joseph

APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
TITLE OF INVENTION: RECEPTOR
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693.697
FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-0037-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 898 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-693-697-36

Query Match 99.1%; Score 4325; DB 2; Length 898;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPTTPWRFKLSQMPNPNSTYDYFLLPAGLSKNTSNS 60
DB 3 MICQKFCVLLHWEFIYVITAFNLSYPTTPWRFKLSQMPNPNSTYDYFLLPAGLSKNTSNS 62

QY 61 NGHYETAPEPKFNSGTHFSNLSKTTFHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 120
DB 63 NGHYETAPEPKFNSGTHFSNLSKATFHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 122

QY 121 QIDANNIOCWLGDKLKFICYVESLFKNLFNRYNFKVHLLVYLPVLEDSPLVPQKGS 180
DB 123 QIDANNIOCWLGDKLKFICYVESLFKNLFNRYNFKVHLLVYLPVLEDSPLVPQKGS 182

QY 181 FQVHCNCSVHECCVLPVPTAKLNDTLMLCKITSGVIFQSPPLMSVQPINMKVDPDP 240
DB 183 FQVHCNCSVHECCVLPVPTAKLNDTLMLCKITSGVIFQSPPLMSVQPINMKVDPDP 242

QY 241 LGLHMEITDDGNLKSWSPPPLVPPLOQYQVYKYSNSTTVIREADKIVSATSLLVDSILP 300
DB 243 LGLHMEITDDGNLKSWSPPPLVPPLOQYQVYKYSNSTTVIREADKIVSATSLLVDSILP 302

QY 301 GSSYEVOVRKRLDGGPGIWSDNSTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKNKI 360
DB 303 GSSYEVOVRKRLDGGPGIWSDNSTPRVFTTQDVYIFPPKILTSVGSNVSFHCYKKNKI 362

QY 361 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFNFKNETKPRGKFTYDAVYCCNEHECHH 420
DB 363 VPSKEIYVMMNLAEKIPQSOYDVVSDHVSQVTFNFKNETKPRGKFTYDAVYCCNEHECHH 422

QY 421 RYAEIYVIVDWININISCTDGYLTMTKCRNSTSTIQSLAESTLQRLYHRSSLYCSDIPSIIH 480

Db 423 RYAEIYVIDVNIINISCTDGYLTKMTCRWSTSIQSLAESTLQLRHRSLSYCDIPSIH 482
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVRKPLPP 540
Db 483 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVRKPLPP 542
QY 541 SSVKAEITINIGLLKISWEKPVPPENNLOFQIRYGLSGKEVQWKMYEYDAKSKVSLPV 600
Db 543 SSVKAEITINIGLLKISWEKPVPPENNLOFQIRYGLSGKEVQWKMYEYDAKSKVSLPV 602
QY 601 PDLCAVAVQVRCKRLDGLGYWSNPNATVYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 603 PDLCAVAVQVRCKRLDGLGYWSNPNATVYVMDIKVPMRGPEFWRIINGDTMKKEKNV 662
QY 661 TLLWKLPMKNDLSLCSVQRYVINHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 663 TLLWKLPMKNDLSLCSVQRYVINHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780
Db 723 GASVANFNLTFSWPMKVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 782
QY 781 GEIKWLRISSSVKYYIHGKF 801
Db 783 GEIKWLRISSSVKYYIHDF 803

RESULT 3

US-08-693-697-33

; Sequence 33, Application US/08693697

; Patent No. 5869610

; GENERAL INFORMATION:

; APPLICANT: Snodgrass, H. R.

; APPLICANT: Cioffi, Joseph

; APPLICANT: Zupancic, Thomas J.

; APPLICANT: Shafer, Alan W.

; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: FastSeq for Windows Version 2.0b

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/693,697

; FILING DATE: 05-AUG-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Polissant, Brian M.

; REGISTRATION NUMBER: 28,462

; REFERENCE/DOCKET NUMBER: 8907-0037-999

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-493-4935

; TELEFAX: 650-493-5556

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 908 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal

; US-08-693-697-33

Query Match 99.1%; Score 4325; DB 2; Length 908;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICOKFCVLLHWEFYIVITAFNLSPITPWRFKLSKMPNPNSTYDYFLLPAGLSKNTS 60

Db 3 MICOKFCVLLHWEFYIVITAFNLSPITPWRFKLSKMPNPNSTYDYFLLPAGLSKNTS 62

QY 61 NGHYETAPEPKFNSSSTHFNLSKTTFFHCCFRSEQRNCSLACADNTEGKTFVTVNSLVP 120

Db 63 NGHYETAPEPKFNSSSTHFNLSKTTFFHCCFRSEQRNCSLACADNTEGKTFVTVNSLVP 122

QY 121 QQIDANNITQCLWLGDLKLFICYVESLFKNLFNRYNKKVHLLVLPVLEDSPLVPQKGS 180

Db 123 QQIDANNITQCLWLGDLKLFICYVESLFKNLFNRYNKKVHLLVLPVLEDSPLVPQKGS 182

QY 181 FQVHCNCSVHECCCLVPPVPTAKLNDTLLMCLKITSGGVIFOSPLMSVQPINNVKPDPP 240

Db 183 FQVHCNCSVHECCCLVPPVPTAKLNDTLLMCLKITSGGVIFOSPLMSVQPINNVKPDPP 242

QY 241 LGLHMEITDDGNLKIWSPPPLVPFPLOVQVYKSENSTTVIREADKIVSATSLVDSILP 300

Db 243 LGLHMEITDDGNLKIWSPPPLVPFPLOVQVYKSENSTTVIREADKIVSATSLVDSILP 302

QY 301 GSSYEYQVRGKRLDGPGLWSNDSWSTPRVFTTQDVIYPPPKILTSVGNVSPFHCYKKNKI 360

Db 303 GSSYEYQVRGKRLDGPGLWSNDSWSTPRVFTTQDVIYPPPKILTSVGNVSPFHCYKKNKI 362

QY 361 VPSKEIVWMNLAETIPQSOYDVVSDHVSKVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420

Db 363 VPSKEIVWMNLAETIPQSOYDVVSDHVSKVTFEFLNETKPRGKFTYDAVYCCNEHECHH 422

QY 421 RYAEIYVIDVNIINISCTDGYLTKMTCRWSTSIQSLAESTLQLRHRSLSYCDIPSIH 480

Db 423 RYAEIYVIDVNIINISCTDGYLTKMTCRWSTSIQSLAESTLQLRHRSLSYCDIPSIH 482

QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVRKPLPP 540

Db 483 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVRKPLPP 542

QY 541 SSVKAEITINIGLLKISWEKPVPPENNLOFQIRYGLSGKEVQWKMYEYDAKSKVSLPV 600

Db 543 SSVKAEITINIGLLKISWEKPVPPENNLOFQIRYGLSGKEVQWKMYEYDAKSKVSLPV 602

QY 601 PDLCAVAVQVRCKRLDGLGYWSNPNATVYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

Db 603 PDLCAVAVQVRCKRLDGLGYWSNPNATVYVMDIKVPMRGPEFWRIINGDTMKKEKNV 662

QY 661 TLLWKLPMKNDLSLCSVQRYVINHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720

Db 663 TLLWKLPMKNDLSLCSVQRYVINHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 722

QY 721 GASVANFNLTFSWPMKVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 780

Db 723 GASVANFNLTFSWPMKVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMYFIEWKNLNED 782

QY 781 GEIKWLRISSSVKYYIHGKF 801

Db 783 GEIKWLRISSSVKYYIHDF 803

RESULT 4

US-08-355-888A-8

; Sequence 8, Application US/08355888A

; Patent No. 5763211

; GENERAL INFORMATION:

; APPLICANT: Snodgrass, H. R.

; APPLICANT: Cioffi, Joseph

; APPLICANT: Zupancic, Thomas J.

; APPLICANT: Shafer, Alan W.

; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN

```

; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/355,888A
; FILING DATE: 14-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7225-078
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 960 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-355-888A-8

Query Match 99.1%; Score 4325; DB 1; Length 960;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEIYVITAFNLSPYTPWRFKLSCLMPPNSTYDFLLPAGLSKNTSNS 60
DB 3 MICQKFCVLLHWEIYVITAFNLSPYTPWRFKLSCLMPPNSTYDFLLPAGLSKNTSNS 62
QY 61 NGHYETAVEPKFNSGTHFNSLKTFFCCPSEODRNCISLCAADNIEGKTFVSTVNSLVF 120
DB 63 NGHYETAVEPKFNSGTHFNSLKTFFCCPSEODRNCISLCAADNIEGKTFVSTVNSLVF 122
QY 121 QOIDANNIOCLWGLDLKLFICYVESLEKFLFRNYNYKVHLLYLVPEVLESPLVPQKGS 180
DB 123 QOIDANNIOCLWGLDLKLFICYVESLEKFLFRNYNYKVHLLYLVPEVLESPLVPQKGS 182
QY 181 FQVHCNCSVHECCCLVPVPTAKLNDLMLCLKITSGVIFQSPMSVQPINNVKPDPP 240
DB 183 FQVHCNCSVHECCCLVPVPTAKLNDLMLCLKITSGVIFQSPMSVQPINNVKPDPP 242
QY 241 LGLHMETDDGNLKSISPPPLFPFQYQVYKYSNSTVTVREADKIVSATSLVDSILP 300
DB 243 LGLHMETDDGNLKSISPPPLFPFQYQVYKYSNSTVTVREADKIVSATSLVDSILP 302
QY 301 GSSYEYQVGRKRLDGLGYSWNSNPAYTVVMDIKVPMRGPFWRIINGDTMKKERNV 360
DB 303 GSSYEYQVGRKRLDGLGYSWNSNPAYTVVMDIKVPMRGPFWRIINGDTMKKERNV 362
QY 361 VPSKEIYVNMNLAEKIPQSDYVSDHVSQVTFNLAETKPRGFTYDAVYCCNEHECHH 420
DB 363 VPSKEIYVNMNLAEKIPQSDYVSDHVSQVTFNLAETKPRGFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVYDYNINISCTDGYLTWMTCRWSTSTTQSLAESTLQRYHRSSLYCSDIPSII 480
DB 423 RYAEIYVYDYNINISCTDGYLTWMTCRWSTSTTQSLAESTLQRYHRSSLYCSDIPSII 482
QY 481 PISEPKDCYVLDQSGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
DB 483 PISEPKDCYVLDQSGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQMKMYEYVYDAKSYSVSLPV 600
DB 543 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQMKMYEYVYDAKSYSVSLPV 602
QY 601 PDLCAVYAVQVRCKRLDGLGYSWNSNPAYTVVMDIKVPMRGPFWRIINGDTMKKERNV 660
DB 603 PDLCAVYAVQVRCKRLDGLGYSWNSNPAYTVVMDIKVPMRGPFWRIINGDTMKKERNV 662
QY 661 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSYEDVGNHTKFTFLTEQAHTVTVLAINSI 720
DB 663 TLLWKPLMKNDSLCSVQRYVINHHTSCNGTWSYEDVGNHTKFTFLTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKSNVIVOSLSAYPLNNSCVIVSWILSPSDYKLMYFIIEWKNLND 780
DB 723 GASVANFNLTFSWPMKSNVIVOSLSAYPLNNSCVIVSWILSPSDYKLMYFIIEWKNLND 782
QY 781 GEIKWLRISSSVKKYIHKGF 801
DB 783 GEIKWLRISSSVKKYIHDHF 803

RESULT 5
US-08-693-697-8
; Sequence 8, Application US/08693697
; Patent No. 5869610
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693,697
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0037-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 960 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-693-697-8

Query Match 99.1%; Score 4325; DB 2; Length 960;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEIYVITAFNLSPYTPWRFKLSCLMPPNSTYDFLLPAGLSKNTSNS 60
DB 3 MICQKFCVLLHWEIYVITAFNLSPYTPWRFKLSCLMPPNSTYDFLLPAGLSKNTSNS 62
QY 61 NGHYETAVEPKFNSGTHFNSLKTFFCCPSEODRNCISLCAADNIEGKTFVSTVNSLVF 120
DB 63 NGHYETAVEPKFNSGTHFNSLKTFFCCPSEODRNCISLCAADNIEGKTFVSTVNSLVF 122
QY 121 QOIDANNIOCLWGLDLKLFICYVESLEKFLFRNYNYKVHLLYLVPEVLESPLVPQKGS 180
DB 123 QOIDANNIOCLWGLDLKLFICYVESLEKFLFRNYNYKVHLLYLVPEVLESPLVPQKGS 182
QY 181 FQVHCNCSVHECCCLVPVPTAKLNDLMLCLKITSGVIFQSPMSVQPINNVKPDPP 240
DB 183 FQVHCNCSVHECCCLVPVPTAKLNDLMLCLKITSGVIFQSPMSVQPINNVKPDPP 242
QY 241 LGLHMETDDGNLKSISPPPLFPFQYQVYKYSNSTVTVREADKIVSATSLVDSILP 300
DB 243 LGLHMETDDGNLKSISPPPLFPFQYQVYKYSNSTVTVREADKIVSATSLVDSILP 302
QY 301 GSSYEYQVGRKRLDGLGYSWNSNPAYTVVMDIKVPMRGPFWRIINGDTMKKERNV 360
DB 303 GSSYEYQVGRKRLDGLGYSWNSNPAYTVVMDIKVPMRGPFWRIINGDTMKKERNV 362
QY 361 VPSKEIYVNMNLAEKIPQSDYVSDHVSQVTFNLAETKPRGFTYDAVYCCNEHECHH 420
DB 363 VPSKEIYVNMNLAEKIPQSDYVSDHVSQVTFNLAETKPRGFTYDAVYCCNEHECHH 422
QY 421 RYAEIYVYDYNINISCTDGYLTWMTCRWSTSTTQSLAESTLQRYHRSSLYCSDIPSII 480
DB 423 RYAEIYVYDYNINISCTDGYLTWMTCRWSTSTTQSLAESTLQRYHRSSLYCSDIPSII 482
QY 481 PISEPKDCYVLDQSGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
DB 483 PISEPKDCYVLDQSGFYECIFQPIFLLSGYTMWIRINHSLGSLDSPPTCVLPDSVVKPLPP 542

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Db 3 MICQFCVLLHWEFYIVITAFNLSYPTIPWRFKLSGMPNPNSTYDFLLPAGLSKNTS 62
QY 61 NGHETAVEPKFNSSGTHFNSLSTTFCFRSDQNRNCSLCADNIEGKTFVSTVNSLVF 120
Db 63 NGHETAVEPKFNSSGTHFNSLSTTFCFRSDQNRNCSLCADNIEGKTFVSTVNSLVF 122
QY 121 QOIDANNIOCLWGLDKLFCYVESLFKLFNRYNKVHLLYLVPEVLEDSPLVPQKGS 180
Db 123 QOIDANNIOCLWGLDKLFCYVESLFKLFNRYNKVHLLYLVPEVLEDSPLVPQKGS 182
QY 181 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPVLSVOPINNVKPDPP 240
Db 183 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPVLSVOPINNVKPDPP 242
QY 241 LGLHMETDGNLKIWSNPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLVDSILP 300
Db 243 LGLHMETDGNLKIWSNPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLVDSILP 302
QY 301 GSSYEVOVRKRLDGGPGIWSDMSTPRVFTQDVIYFPFKILTSGVNSVPHCIYKKNKI 360
Db 303 GSSYEVOVRKRLDGGPGIWSDMSTPRVFTQDVIYFPFKILTSGVNSVPHCIYKKNKI 362
QY 361 VPSKEIWMNLAEKIPQSOQYDVVSDHVSKVTFEFLNETKPRGKFTYDGVCCNEHECHH 420
Db 363 VPSKEIWMNLAEKIPQSOQYDVVSDHVSKVTFEFLNETKPRGKFTYDGVCCNEHECHH 422
QY 421 RYAEIYVIDVNIINISCTDGYLTMTKTCRWSSTTQSLAESTLQLRVHRSLSYCDIPSIH 480
Db 423 RYAEIYVIDVNIINISCTDGYLTMTKTCRWSSTTQSLAESTLQLRVHRSLSYCDIPSIH 482
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVRPLPP 540
Db 483 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVRPLPP 542
QY 541 SSVKAEITINIGLLKISWEKPVPEPENNLOFQIRYGLSGKEVQWKMYEVDKSKSVSLPV 600
Db 543 SSVKAEITINIGLLKISWEKPVPEPENNLOFQIRYGLSGKEVQWKMYEVDKSKSVSLPV 602
QY 601 PDLCAVAVQVRKRLDGLGYSWNSNPAYTVVMDIKVPMRGPEFWIRIINGDTMKKEKNV 660
Db 603 PDLCAVAVQVRKRLDGLGYSWNSNPAYTVVMDIKVPMRGPEFWIRIINGDTMKKEKNV 662
QY 661 TLLWKLPMKNDLSQVQRYVINHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 663 TLLWKLPMKNDLSQVQRYVINHTSCNGTWSEDVGNHTKFTFLWTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKVNIVQSLSATPLNSSCVIVSWILSPSDYKLMYFIIEMKNLNE 780
Db 723 GASVANFNLTFSWPMKVNIVQSLSATPLNSSCVIVSWILSPSDYKLMYFIIEMKNLNE 782
QY 781 GEIKWLRISSSVKYYIHGRF 801
Db 783 GEIKWLRISSSVKYYIHDHF 803

RESULT 6

US-08-640-389A-3

; Sequence 3, Application US/08640389A

; Patent No. 5912123

; GENERAL INFORMATION:

; APPLICANT: Snodgrass, H. R.

; APPLICANT: Cioffi, Joseph

; APPLICANT: Zupancic, Thomas J.

; APPLICANT: Shafer, Alan W.

; TITLE OF INVENTION: DETECTION OF THE LEPTIN

; TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR

; TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,389A
FILING DATE: 29-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-640-389A-3

Query Match 99.1%; Score 4325; DB 2; Length 960;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICQFCVLLHWEFYIVITAFNLSYPTIPWRFKLSGMPNPNSTYDFLLPAGLSKNTS 60

Db 3 MICQFCVLLHWEFYIVITAFNLSYPTIPWRFKLSGMPNPNSTYDFLLPAGLSKNTS 62

QY 61 NGHETAVEPKFNSSGTHFNSLSTTFCFRSDQNRNCSLCADNIEGKTFVSTVNSLVF 120

Db 63 NGHETAVEPKFNSSGTHFNSLSTTFCFRSDQNRNCSLCADNIEGKTFVSTVNSLVF 122

QY 121 QOIDANNIOCLWGLDKLFCYVESLFKLFNRYNKVHLLYLVPEVLEDSPLVPQKGS 180

Db 123 QOIDANNIOCLWGLDKLFCYVESLFKLFNRYNKVHLLYLVPEVLEDSPLVPQKGS 182

QY 181 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPVLSVOPINNVKPDPP 240

Db 183 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPVLSVOPINNVKPDPP 242

QY 241 LGLHMETDGNLKIWSNPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLVDSILP 300

Db 243 LGLHMETDGNLKIWSNPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLVDSILP 302

QY 301 GSSYEVOVRKRLDGGPGIWSDMSTPRVFTQDVIYFPFKILTSGVNSVPHCIYKKNKI 360

Db 303 GSSYEVOVRKRLDGGPGIWSDMSTPRVFTQDVIYFPFKILTSGVNSVPHCIYKKNKI 362

QY 361 VPSKEIWMNLAEKIPQSOQYDVVSDHVSKVTFEFLNETKPRGKFTYDGVCCNEHECHH 420

Db 363 VPSKEIWMNLAEKIPQSOQYDVVSDHVSKVTFEFLNETKPRGKFTYDGVCCNEHECHH 422

QY 421 RYAEIYVIDVNIINISCTDGYLTMTKTCRWSSTTQSLAESTLQLRVHRSLSYCDIPSIH 480

Db 423 RYAEIYVIDVNIINISCTDGYLTMTKTCRWSSTTQSLAESTLQLRVHRSLSYCDIPSIH 482

QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVRPLPP 540

Db 483 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVRPLPP 542

QY 541 SSVKAEITINIGLLKISWEKPVPEPENNLOFQIRYGLSGKEVQWKMYEVDKSKSVSLPV 600

Db 543 SSVKAEITINIGLLKISWEKPVPEPENNLOFQIRYGLSGKEVQWKMYEVDKSKSVSLPV 602

QY 601 PDLCAVAVQVRCRDLGLGYWNSNPNAYTVVMDIKVPMRGPEFWRIINGDPMKKEKNV 660
DB 603 PDLCAVAVQVRCRDLGLGYWNSNPNAYTVVMDIKVPMRGPEFWRIINGDPMKKEKNV 662
QY 661 TLLWKLPMKNDLSLCSVQRYVINHTSCNGTWSVDGNGHKTFTFLWTEQAHTVTVLAINSI 720
DB 663 TLLWKLPMKNDLSLCSVQRYVINHTSCNGTWSVDGNGHKTFTFLWTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKSNVIVQSLAYPLNSSCVIVSWILSPDYKLMYFIIEMKLNED 780
DB 723 GASVANFNLTFSWPMKSNVIVQSLAYPLNSSCVIVSWILSPDYKLMYFIIEMKLNED 782
QY 781 GEIKWLRISSSVKYYIHGKF 801
DB 783 GEIKWLRISSSVKYYIHDF 803

RESULT 7

US-08-693-696-8
; Sequence 8, Application US/08693696
; Patent No. 6005080

GENERAL INFORMATION:

; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cloffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: Hu-B1.219, A NOVEL HUMAN HEMATOPOIETIN
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/693.696
; FILING DATE:

CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/355,888
; FILING DATE: 14-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 7225-078
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO:

8:

SEQUENCE CHARACTERISTICS:

LENGTH: 960 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-693-696-8

Query Match

Best Local Similarity 99.18; Score 4325; DB 3; Length 960;

Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIVITAFNLSYPTTPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60

DB 3 MICQKFCVLLHWEFIVITAFNLSYPTTPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 62

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QY 121 QOIDANWNTQWLKGDCLKFICYVESLFPKLNFRNFKVHLLYVLPVLEDSPLVPQKGS 180
DB 123 QOIDANWNTQWLKGDCLKFICYVESLFPKLNFRNFKVHLLYVLPVLEDSPLVPQKGS 182
QY 181 FQMVHCNCSVHECCCLVPPTAKLNDTLLMCLKITSGVIFQSPMLSVQPINNVKPPDP 240
DB 183 FQMVHCNCSVHECCCLVPPTAKLNDTLLMCLKITSGVIFQSPMLSVQPINNVKPPDP 242
QY 241 LGLHMEITDGNLKIWSWSPPLVPFPLOVQVKSNSNTTVIREADKIYSATSLLVDSILP 300
DB 243 LGLHMEITDGNLKIWSWSPPLVPFPLOVQVKSNSNTTVIREADKIYSATSLLVDSILP 302
QY 301 GSSYEVQVRGKRLDGPGLWSDWSTPRVFTQDVYIFPPPKILTSVGSNVSFHCIIYKKNKI 360
DB 303 GSSYEVQVRGKRLDGPGLWSDWSTPRVFTQDVYIFPPPKILTSVGSNVSFHCIIYKKNKI 362
QY 361 VPSKEIVMMNLAEKIPOSXDYDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNHECHH 420
DB 363 VPSKEIVMMNLAEKIPOSXDYDVSDHVSQVTFNLTNETKPRGKFTYDAVYCCNHECHH 422
QY 421 RYAEIYVIDVNIINISCTDGYLTMTCTWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIH 480
DB 423 RYAEIYVIDVNIINISCTDGYLTMTCTWSTSTIQSLAESTLQRLYHRSSLYCSDIPSIH 482
QY 481 PISEPKDCYLQSDGFEYECIFQPIFLLSGYTMWIRNHSGLSDSPPTCVLPDSVVKPLPP 540
DB 483 PISEPKDCYLQSDGFEYECIFQPIFLLSGYTMWIRNHSGLSDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSKEVQWKMYEYDASKSVSLPV 600
DB 543 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSKEVQWKMYEYDASKSVSLPV 602
QY 601 PDLCAVAVQVRCRDLGLGYWNSNPNAYTVVMDIKVPMRGPEFWRIINGDPMKKEKNV 660
DB 603 PDLCAVAVQVRCRDLGLGYWNSNPNAYTVVMDIKVPMRGPEFWRIINGDPMKKEKNV 662
QY 661 TLLWKLPMKNDLSLCSVQRYVINHTSCNGTWSVDGNGHKTFTFLWTEQAHTVTVLAINSI 720
DB 663 TLLWKLPMKNDLSLCSVQRYVINHTSCNGTWSVDGNGHKTFTFLWTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKSNVIVQSLAYPLNSSCVIVSWILSPDYKLMYFIIEMKLNED 780
DB 723 GASVANFNLTFSWPMKSNVIVQSLAYPLNSSCVIVSWILSPDYKLMYFIIEMKLNED 782
QY 781 GEIKWLRISSSVKYYIHGKF 801
DB 783 GEIKWLRISSSVKYYIHDF 803

RESULT 8

US-08-588-190-3
; Sequence 3, Application US/08588190
; Patent No. 5856098

GENERAL INFORMATION:

; APPLICANT: Snodgrass, H. Ralph
; APPLICANT: Cloffi, Joseph
; APPLICANT: Zupancic, Thomas Joel
; APPLICANT: Shafer, Alan Wayne
; TITLE OF INVENTION: DETECTION OF A LEPTIN RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811

COMPUTER READABLE FORM:

;

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,190
FILING DATE: 18-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 008907-0029-999
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-588-190-3

Query Match 99.0%; Score 4320; DB 2; Length 960;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 795; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFYIVTAFLNLSYPTIPWRFKLSMPPNPNSTYDFLLPAGLSKNTS 60
DB 3 MICQKFCVLLHWEFYIVTAFLNLSYPTIPWRFKLSMPPNPNSTYDFLLPAGLSKNTS 62
QY 61 NGHYETAVEPKNSCTHFSNLSKTFHCCFSEQDRNCSLCADNTEGTFVSTVNSLVF 120
DB 63 NGHYETAVEPKNSCTHFSNLSKATFHCFCFSEQDRNCSLCADNTEGTFVSTVNSLVF 122
QY 121 QQIDANNIQCWLKGLKLFICYVESLFLNRYNYKVHLLYVLEVDSPVLPQKGS 180
DB 123 QQIDANNIQCWLKGLKLFICYVESLFLNRYNYKVHLLYVLEVDSPVLPQKGS 182
QY 181 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGVIFOSPLMSVQPINMVKPDP 240
DB 183 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGVIFOSPLMSVQPINMVKPDP 242
QY 241 LGLHMEITDGNLKITSSWSPPLVPVPPLOVQVYSENSTTVIREADKIVSATSLVDSILP 300
DB 243 LGLHMEITDGNLKITSSWSPPLVPVPPLOVQVYSENSTTVIREADKIVSATSLVDSILP 302
QY 301 GSSYEVQVGRKLDGPGINSDMSTPRVFTQDVYVPPPKILTSGVSNVSHFCIYKKNKI 360
DB 303 GSSYEVQVGRKLDGPGINSDMSTPRVFTQDVYVPPPKILTSGVSNVSHFCIYKKNKI 362
QY 361 VPSKEIVWNNIAEKIPQSQYQVSDHVSQVTFNNETKPKGFTYDQVYCCNEHECHH 420
DB 363 VPSKEIVWNNIAEKIPQSQYQVSDHVSQVTFNNETKPKGFTYDQVYCCNEHECHH 422
QY 421 RYAEIVYDVNINISCTDGYLTCTCRKSTSTIQSLAESTLQLRHRSLSYCSIDPSIH 480
DB 423 RYAEIVYDVNINISCTDGYLTCTCRKSTSTIQSLAESTLQLRHRSLSYCSIDPSIH 482
QY 481 PISEPKDCYQSDGVECFIQIFILLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
DB 483 PISEPKDCYQSDGVECFIQIFILLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGREVQMKVEYVDAKSKSVSLPV 600
DB 543 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGREVQMKVEYVDAKSKSVSLPV 602

QY 601 PDLCAVYAVQVRCKRLDGLGYWSNNSNPAYTVVMDIKVPMRGPEFWRRIINGDTMKKEKNV 660
DB 603 PDLCAVYAVQVRCKRLDGLGYWSNNSNPAYTVVMDIKVPMRGPEFWRRIINGDTMKKEKNV 662
QY 661 TLLWKPLMKNDLSLCSVORYVINHTSCNCTWSEDVGNHKTFTLWTEQAHVTVLAINSI 720
DB 663 TLLWKPLMKNDLSLCSVORYVINHTSCNCTWSEDVGNHKTFTLWTEQAHVTVLAINSI 722
QY 721 GASVANENLTFSWPMKVNIVQSLAYSAYPLNSCVIVSWILSPSDYKLYMFIIEWKNLND 780
DB 723 GASVANENLTFSWPMKVNIVQSLAYSAYPLNSCVIVSWILSPSDYKLYMFIIEWKNLND 782
QY 781 GEIKWLRISSSVKYYIHGKF 801
DB 783 GEIKWLRISSSVKYYIHDF 803

RESULT 9
US-08-588-526-3
Sequence 3, Application US/08588526
Patent No. 5882860
GENERAL INFORMATION:
APPLICANT: Snodgrass, H.
APPLICANT: Cloutier, Joseph
APPLICANT: Zupancic, Thomas
APPLICANT: Shafer, Alan
TITLE OF INVENTION: DETECTION OF A LEPTIN RECEPTOR
TITLE OF INVENTION: VARIANT
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
CITY: New York
STATE: New York
COUNTRY: US
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,526
FILING DATE: 18-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 908 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-588-526-3

Query Match 98.9%; Score 4315; DB 2; Length 908;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 794; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFYIVTAFLNLSYPTIPWRFKLSMPPNPNSTYDFLLPAGLSKNTS 60
DB 3 MICQKFCVLLHWEFYIVTAFLNLSYPTIPWRFKLSMPPNPNSTYDFLLPAGLSKNTS 62
QY 61 NGHYETAVEPKNSCTHFSNLSKTFHCCFSEQDRNCSLCADNTEGTFVSTVNSLVF 120

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Db 63 NGHETAVEPEKFNSSGTHFNSLKHATFHCCFRSEQDRNCSLCADNIEGRFTVSTVNSLVF 122
QY 121 QOIDDANNIOCWLGDKLFCYVESLFKRLFRNYKVHLLVYLPEVLEDSPLVPQKGS 180
Db 123 QOIDDANNIOCWLGDKLFCYVESLFKRLFRNYKVHLLVYLPEVLEDSPLVPQKGS 182
QY 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITSGGVIFQSPMLSVQPINNVKPDPP 240
Db 183 FQMVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITSGGVIFQSPMLSVQPINNVKPDPP 242
QY 241 LGLHMETDDGNLKIWSPPPLVPFPLOQYQVYSENSTTVIRADKIVSATSLVDSILP 300
Db 243 LGLHMETDDGNLKIWSPPPLVPFPLOQYQVYSENSTTVIRADKIVSATSLVDSILP 302
QY 301 GSSYEVOVRGRKLDGPGIWSDWSTPRVFTTQDVYIPPKILTSGVSNVSHFCIYKKNKI 360
Db 303 GSSYEVOVRGRKLDGPGIWSDWSTPRVFTTQDVYIPPKILTSGVSNVSHFCIYKKNKI 362
QY 361 VPSKEIYVWNNLAEKIPQSOYDVVSDHVSQVTFNENLTKPRGKFTYDAYCCNEHECHH 420
Db 363 VPSKEIYVWNNLAEKIPQSOYDVVSDHVSQVTFNENLTKPRGKFTYDAYCCNEHECHH 422
QY 421 RYAEIYVIDVNIINISCTDGYLTMTKRWSTSTIQSLAESTLQLRVHRSSLYCSDIPSIH 480
Db 423 RYAEIYVIDVNIINISCTDGYLTMTKRWSTSTIQSLAESTLQLRVHRSSLYCSDIPSIH 482
QY 481 PISEPKDCYLOSDGFEYECIFQPIFLLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLPP 540
Db 483 PISEPKDCYLOSDGFEYECIFQPIFLLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLPP 542
QY 541 SSVKAEITINTGLLKISWEKPVFPENNLIQFQIRYGLSGKEVQWKNYEVYDAKSKSVSLPV 600
Db 543 SSVKAEITINTGLLKISWEKPVFPENNLIQFQIRYGLSGKEVQWKNYEVYDAKSKSVSLPV 602
QY 601 POLCAVYAVQVRCKRLDGLGYWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 603 POLCAVYAVQVRCKRLDGLGYWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 662
QY 661 TLLWRLPLMKNDSCSVQRYVNIHHTSCNGTWSGVNHTKFTFLTEQAHTVTVLAINSI 720
Db 663 TLLWRLPLMKNDSCSVQRYVNIHHTSCNGTWSGVNHTKFTFLTEQAHTVTVLAINSI 722
QY 721 GASVANFNLTFSWPMKYNIVQSLAYSAYPLNCSCTVSWILSPSDYKMLYFIEWKNLNED 780
Db 723 GASVANFNLTFSWPMKYNIVQSLAYSAYPLNCSCTVSWILSPSDYKMLYFIEWKNLNED 782
QY 781 GEIKWLRISSSVKYYIHGKF 801
Db 783 GEIKWLRISSSVKYYIHDF 803

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RESULT 10

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US-08-640-389A-11
; Sequence 11, Application US/08640389A
; Patent No. 5912123

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GENERAL INFORMATION:

```

; APPLICANT: Snodgrass, H. R.
; APPLICANT: Clotfi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.

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; TITLE OF INVENTION: DETECTION OF THE LEPTIN
; TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
; TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY

```

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; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESS: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York

```

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; COUNTRY: USA
; ZIP: 10036-2711

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1165 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-640-389A-11

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Query Match 98.8%; Score 4309; DB 2; Length 1165;
Best Local Similarity 99.1%; Pred. No. 0;
Matches 794; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 1 MICQKFCVLLHWEIYVITAFNLSPITPWRFLKSCMPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEIYVITAFNLSPITPWRFLKSCMPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHETAVEPEKFNSSGTHFNSLKHATFHCCFRSEQDRNCSLCADNIEGRFTVSTVNSLVF 120
Db 61 NGHETAVEPEKFNSSGTHFNSLKHATFHCCFRSEQDRNCSLCADNIEGRFTVSTVNSLVF 120
QY 121 QOIDDANNIOCWLGDKLFCYVESLFKRLFRNYKVHLLVYLPEVLEDSPLVPQKGS 180
Db 121 QOIDDANNIOCWLGDKLFCYVESLFKRLFRNYKVHLLVYLPEVLEDSPLVPQKGS 180
QY 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITSGGVIFQSPMLSVQPINNVKPDPP 240
Db 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITSGGVIFQSPMLSVQPINNVKPDPP 240
QY 241 LGLHMETDDGNLKIWSPPPLVPFPLOQYQVYSENSTTVIRADKIVSATSLVDSILP 300
Db 241 LGLHMETDDGNLKIWSPPPLVPFPLOQYQVYSENSTTVIRADKIVSATSLVDSILP 300
QY 301 GSSYEVOVRGRKLDGPGIWSDWSTPRVFTTQDVYIPPKILTSGVSNVSHFCIYKKNKI 360
Db 301 GSSYEVOVRGRKLDGPGIWSDWSTPRVFTTQDVYIPPKILTSGVSNVSHFCIYKKNKI 360
QY 361 VPSKEIYVWNNLAEKIPQSOYDVVSDHVSQVTFNENLTKPRGKFTYDAYCCNEHECHH 420
Db 361 VPSKEIYVWNNLAEKIPQSOYDVVSDHVSQVTFNENLTKPRGKFTYDAYCCNEHECHH 420
QY 421 RYAEIYVIDVNIINISCTDGYLTMTKRWSTSTIQSLAESTLQLRVHRSSLYCSDIPSIH 480
Db 421 RYAEIYVIDVNIINISCTDGYLTMTKRWSTSTIQSLAESTLQLRVHRSSLYCSDIPSIH 480
QY 481 PISEPKDCYLOSDGFEYECIFQPIFLLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLOSDGFEYECIFQPIFLLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINTGLLKISWEKPVFPENNLIQFQIRYGLSGKEVQWKNYEVYDAKSKSVSLPV 600
Db 541 SSVKAEITINTGLLKISWEKPVFPENNLIQFQIRYGLSGKEVQWKNYEVYDAKSKSVSLPV 600
QY 601 POLCAVYAVQVRCKRLDGLGYWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 POLCAVYAVQVRCKRLDGLGYWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660

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QY 661 TLLWPLMKNDLSVQRYVINHTSCNCTWSDVGNHTKFTFLWTEQAHVTVLAINSI 720
DB 661 TLLWPLMKNDLSVQRYVINHTSCNCTWSDVGNHTKFTFLWTEQAHVTVLAINSI 720
QY 721 GASVANFNLTFSPMKSVMKNIVQSLSAAYPLNASSCVIVSWILSPSDYKLMVFIIEKKNLNE 780
DB 721 GASVANFNLTFSPMKSVMKNIVQSLSAAYPLNASSCVIVSWILSPSDYKLMVFIIEKKNLNE 780
QY 781 GEIKWLRISSSVKYYIHGKF 801
DB 781 GEIKWLRISSSVKYYIHDF 801

RESULT 11

US-08-640-389A-10
; Sequence 10, Application US/08640389A
; Patent No. 5912123
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: DETECTION OF THE LEPTIN
; TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
; TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,389A
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 896 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-640-389A-10

Query Match 98.5%; Score 4297; DB 2; Length 896;
Best Local Similarity 98.8%; Pred No. 0;
Matches 791; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFYITAFNLSPYTPWRFKLSMPNPNSTYDFLLPAGLSKNTSNS 60
DB 1 MICQKFCVLLHWEFYITAFNLSPYTPWRFKLSMPNPNSTYDFLLPAGLSKNTSNS 60
QY 61 NCHYETAVEPKNSGTHFNSLSKTHFCCFRSEQRNCSLADNIEGKTFVSTVNSLVF 120
DB 61 NCHYETAVEPKNSGTHFNSLSKTHFCCFRSEQRNCSLADNIEGKTFVSTVNSLVF 120
QY 121 QQIDANWNIQCWLKGLDLKLFICYVESLFRNFRNYKVHLLYVLPVLEDSPLVPQKGS 180

DB 121 QQIDANWNIQCWLKGLDLKLFICYVESLFRNFRNYKVHLLYVLPVLEDSPLVPQKGS 180
QY 181 FQVHVCNCSVHECCCLVPVPTAKLNDTLMLCKLITSGGVIFQSPKMSVQPINMVKPDP 240
DB 181 FQVHVCNCSVHECCCLVPVPTAKLNDTLMLCKLITSGGVIFQSPKMSVQPINMVKPDP 240
QY 241 LGLHMEITDDGNLKISWSPPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLLVDSILP 300
DB 241 LGLHMEITDDGNLKISWSPPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEVOVRGKRLDGGIHSNDSSTPRVFTTQDVIYPPPKILTSVGSNWSFHCIIYKKNKI 360
DB 301 GSSYEVOVRGKRLDGGIHSNDSSTPRVFTTQDVIYPPPKILTSVGSNWSFHCIIYKKNKI 360
QY 361 VPSKEIYVWMNLAEKIPQSOYDVVSDHVSQVTFNENLNETKPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIYVWMNLAEKIPQSOYDVVSDHVSQVTFNENLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVININISCTDGYLTMTCTRWSTSTIOSLAESTLQLRYHRSLSYCSIDIPSTH 480
DB 421 RYAEIYVIDVININISCTDGYLTMTCTRWSTSTIOSLAESTLQLRYHRSLSYCSIDIPSTH 480
QY 481 PISEPKDCYLQSDGFEYECIFQPIELLSGYTMMIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYLQSDGFEYECIFQPIELLSGYTMMIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMVEYVDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMVEYVDAKSKSVSLPV 600
QY 601 PDLACVYAVQVRCKRLDGLGYWSNMSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKKNV 660
DB 601 PDLACVYAVQVRCKRLDGLGYWSNMSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKKNV 660
QY 661 TLLWPLMKNDLSVQRYVINHTSCNCTWSDVGNHTKFTFLWTEQAHVTVLAINSI 720
DB 661 TLLWPLMKNDLSVQRYVINHTSCNCTWSDVGNHTKFTFLWTEQAHVTVLAINSI 720
QY 721 GASVANFNLTFSPMKSVMKNIVQSLSAAYPLNASSCVIVSWILSPSDYKLMVFIIEKKNLNE 780
DB 721 GASVANFNLTFSPMKSVMKNIVQSLSAAYPLNASSCVIVSWILSPSDYKLMVFIIEKKNLNE 780
QY 781 GEIKWLRISSSVKYYIHGKF 801
DB 781 GEIKWLRISSSVKYYIHDF 801

RESULT 12

US-08-640-389A-9
; Sequence 9, Application US/08640389A
; Patent No. 5912123
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cioffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: DETECTION OF THE LEPTIN
; TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
; TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/640,389A
;; FILING DATE: 29-APR-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Poissant, Brian M.
;; REGISTRATION NUMBER: 28,462
;; REFERENCE/DOCKET NUMBER: 8907-032
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 906 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-08-640-389A-9

Query Match 98.5%; Score 4297; DB 2; Length 906;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 791; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPTIPWREKLSKMPNSTYDYFLLPAGLSKNTS 60
DB 1 MICQKFCVLLHWEFIYVITAFNLSYPTIPWREKLSKMPNSTYDYFLLPAGLSKNTS 60
QY 61 NGHYETAPEKFNSSGTHFNSLKTTHCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 NGHYETAPEKFNSSGTHFNSLKTTHCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDANNWIOCLWGLKLFICYVESLKNFRNFKVHLLYVLPVLEDSPLVPQKGS 180
DB 121 QQIDANNWIOCLWGLKLFICYVESLKNFRNFKVHLLYVLPVLEDSPLVPQKGS 180
QY 181 FQVHCNCSVHECCCLVPPPTAKNDTLLMCLKITSGGVIFQSPMSVQPINNVKDPDP 240
DB 181 FQVHCNCSVHECCCLVPPPTAKNDTLLMCLKITSGGVIFQSPMSVQPINNVKDPDP 240
QY 241 LGLHMETDGNLAKISWSSPLPFPQYQVKSSENSTTVTREADKIVSATSLVDSILP 300
DB 241 LGLHMETDGNLAKISWSSPLPFPQYQVKSSENSTTVTREADKIVSATSLVDSILP 300
QY 301 GSSYEVOVRKRLDGPISWSDWSTPRVFTTQDVYFPPKILTSVGSNVSPHCYIKKENKI 360
DB 301 GSSYEVOVRKRLDGPISWSDWSTPRVFTTQDVYFPPKILTSVGSNVSPHCYIKKENKI 360
QY 361 VPSKEIYVWNNLAEKIPQSQDYVSDVSHVSKVTFFNLNETPRGKFTYDAVYCCNEHECHH 420
DB 361 VPSKEIYVWNNLAEKIPQSQDYVSDVSHVSKVTFFNLNETPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNIINISCTDGLTKMTCTRWSTSTIOSLAESTLQLRHRSLSYCDIPSIIH 480
DB 421 RYAEIYVIDVNIINISCTDGLTKMTCTRWSTSTIOSLAESTLQLRHRSLSYCDIPSIIH 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTWMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTWMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
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DB 541 SSVKAEITINGLLKISWEKVPENNLQFIQIRYGLSGKEVQNMKEVYDAKSYSVSLPV 600
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DB 601 PDLCAVYAVOVRKRLDGLGYWNSNPATVYMDIKVPMRGPEFRWIRINGDTMKEKNV 660
QY 661 TLLWKPLMKNDLSLCSVQRYVINHTSCNGTWSBDVGNHTKFTFLWTEQAHTVTVLAINSI 720
DB 661 TLLWKPLMKNDLSLCSVQRYVINHTSCNGTWSBDVGNHTKFTFLWTEQAHTVTVLAINSI 720

QY 721 GASVANFNLTFSWPMKSNVIVQSLAYSPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780
DB 721 GASVANFNLTFSWPMKSNVIVQSLAYSPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNE 780
QY 781 GEIKWLRISSSVKKYIYHGF 801
DB 781 GEIKWLRISSSVKKYIYHGF 801

RESULT 13
US-08-640-389A-8
; Sequence 8, Application US/08640389A
; Patent No. 5912123
; GENERAL INFORMATION:
; APPLICANT: Snodgrass, H. R.
; APPLICANT: Cloffi, Joseph
; APPLICANT: Zupancic, Thomas J.
; APPLICANT: Shafer, Alan W.
; TITLE OF INVENTION: DETECTION OF THE LEPTIN
; TITLE OF INVENTION: RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
; TITLE OF INVENTION: REGULATING REPRODUCTIVE BIOLOGY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: - IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; APPLICATION NUMBER: US/08/640,389A
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M.
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 958 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-640-389A-8

Query Match 98.5%; Score 4297; DB 2; Length 958;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 791; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPTIPWREKLSKMPNSTYDYFLLPAGLSKNTS 60
DB 1 MICQKFCVLLHWEFIYVITAFNLSYPTIPWREKLSKMPNSTYDYFLLPAGLSKNTS 60
QY 61 NGHYETAPEKFNSSGTHFNSLKTTHCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 NGHYETAPEKFNSSGTHFNSLKTTHCCFRSEQRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDANNWIOCLWGLKLFICYVESLKNFRNFKVHLLYVLPVLEDSPLVPQKGS 180
DB 121 QQIDANNWIOCLWGLKLFICYVESLKNFRNFKVHLLYVLPVLEDSPLVPQKGS 180

QY 181 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGGVIFQSPPLMSVQPINNVKPDPP 240
Db 181 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGGVIFQSPPLMSVQPINNVKPDPP 240
QY 241 LGLHMETDGNLKIWSPPPLVPFLOQVQKYSNSTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMETDGNLKIWSPPPLVPFLOQVQKYSNSTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEVQVRKRLDGGPGLWSNSTPRVFTQDVIYPPPKILTSGVSNVSHFCIYKKNKI 360
Db 301 GSSYEVQVRKRLDGGPGLWSNSTPRVFTQDVIYPPPKILTSGVSNVSHFCIYKKNKI 360
QY 361 VPSKEIVWMNLAELKIPQSOYDVVSHVSKVTFNENETKPRGKFTYDVCYCCNEHCHH 420
Db 361 VPSKEIVWMNLAELKIPQSOYDVVSHVSKVTFNENETKPRGKFTYDVCYCCNEHCHH 420
QY 421 RYAEIVIDVNIINISCTDGYLTMTKCRWSTSTIOSLAESTLQRLYHRSLSYCDIPSIH 480
Db 421 RYAEIVIDVNIINISCTDGYLTMTKCRWSTSTIOSLAESTLQRLYHRSLSYCDIPSIH 480
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Db 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVPPENNLOFQIRYGLSGKEVQKMYEYVDAKSKVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVPPENNLOFQIRYGLSGKEVQKMYEYVDAKSKVSLPV 600
QY 601 POLCAYAVQVRCKRLDGLGYNSNPNPAYVVMQIKVPMRGPEFWRINGDPMKKEKNV 660
Db 601 POLCAYAVQVRCKRLDGLGYNSNPNPAYVVMQIKVPMRGPEFWRINGDPMKKEKNV 660
QY 661 TLLWPKLMDKNDLSQVQRYVINHTSCNGTWSVDGNHKTFTFLWTEQARTVTVLAINSI 720
Db 661 TLLWPKLMDKNDLSQVQRYVINHTSCNGTWSVDGNHKTFTFLWTEQARTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVIVQSLAYPLNSCVIVSWILSPSDYKLMYFIEWKNLNED 780
Db 721 GASVANFNLTFSWPMKSNVIVQSLAYPLNSCVIVSWILSPSDYKLMYFIEWKNLNED 780
QY 781 GEIKWLRISSVKKYIHGKF 801
Db 781 GEIKWLRISSVKKYIHDF 801

RESULT 14

US-08-640-389A-12
Sequence 12, Application US/08640389A
Patent No. 5912123
GENERAL INFORMATION:
APPLICANT: Snodgrass, H. R.
APPLICANT: Clouff, Joseph
APPLICANT: Zupancic, Thomas J.
APPLICANT: Shafer, Alan W.
TITLE OF INVENTION: DETECTION OF THE LEPTIN
RECEPTOR IN REPRODUCTIVE ORGANS AND METHODS FOR
OPERATING SYSTEM: PC-DOS/MS-DOS
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/640,389A
FILING DATE: 29-APR-1996

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 8907-032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 896 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-640-389A-12

Query Match 77.0%; Score 3361; DB 2; Length 896;

Best Local Similarity 76.2%; Pred. No. 1.2e-299;

Matches 610; Conservative 72; Mismatches 119; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFYVITAFNLSPITPWPKLSCMPNPNSTYDFELLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEFYVITAFNLSPITPWPKLSCMPNPNSTYDFELLPAGLSKNTSNS 60
QY 61 NGHYETAVPEKPNSSCTHFSNLKSTTFHCCESEQRNCSLACADNIEGKTFSTVNSLVF 120
Db 61 KGASEAIVPEKPNSSCTHFSNLKSTTFHCCESEQRNCSLACADNIEGKTFSTVNSLVF 120
QY 121 QOIDANWTOCMLKGDLPICVYVESLFLPNLRYNYKVHLLVLPVLEDSPLVPQKGS 180
Db 121 ROLGVNMDIECMKGDLPICVYVESLFLPNLRYNYKVHLLVLPVLEDSPLVPQKGS 180
QY 181 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGGVIFQSPPLMSVQPINNVKPDPP 240
Db 181 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGGVIFQSPPLMSVQPINNVKPDPP 240
QY 241 LGLHMETDGNLKIWSPPPLVPFLOQVQKYSNSTVIREADKIVSATSLLVDSILP 300
Db 241 LGLHMETDGNLKIWSPPPLVPFLOQVQKYSNSTVIREADKIVSATSLLVDSILP 300
QY 301 GSSYEVQVRKRLDGGPGLWSNSTPRVFTQDVIYPPPKILTSGVSNVSHFCIYKKNKI 360
Db 301 GSSYEVQVRKRLDGGPGLWSNSTPRVFTQDVIYPPPKILTSGVSNVSHFCIYKKNKI 360
QY 361 VPSKEIVWMNLAELKIPQSOYDVVSHVSKVTFNENETKPRGKFTYDVCYCCNEHCHH 420
Db 361 VPSKEIVWMNLAELKIPQSOYDVVSHVSKVTFNENETKPRGKFTYDVCYCCNEHCHH 420
QY 421 RYAEIVIDVNIINISCTDGYLTMTKCRWSTSTIOSLAESTLQRLYHRSLSYCDIPSIH 480
Db 421 RYAEIVIDVNIINISCTDGYLTMTKCRWSTSTIOSLAESTLQRLYHRSLSYCDIPSIH 480
QY 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVPPENNLOFQIRYGLSGKEVQKMYEYVDAKSKVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVPPENNLOFQIRYGLSGKEVQKMYEYVDAKSKVSLPV 600
QY 601 POLCAYAVQVRCKRLDGLGYNSNPNPAYVVMQIKVPMRGPEFWRINGDPMKKEKNV 660
Db 601 POLCAYAVQVRCKRLDGLGYNSNPNPAYVVMQIKVPMRGPEFWRINGDPMKKEKNV 660
QY 661 TLLWPKLMDKNDLSQVQRYVINHTSCNGTWSVDGNHKTFTFLWTEQARTVTVLAINSI 720
Db 661 TLLWPKLMDKNDLSQVQRYVINHTSCNGTWSVDGNHKTFTFLWTEQARTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVIVQSLAYPLNSCVIVSWILSPSDYKLMYFIEWKNLNED 780
Db 721 GASVANFNLTFSWPMKSNVIVQSLAYPLNSCVIVSWILSPSDYKLMYFIEWKNLNED 780

Db 721 GASLVNENLTFSPWMSKVSAYESLSAVPLSSCVLSWTLSPDDYSLLYLVIEWKILNED 780

QY 781 GEIKWLRISSSVKYYTHGKF 801
Db 781 DGMKWLRIPSNVKFFYHDNF 801

RESULT 15
US-08-599-455B-2
Sequence 2, Application US/08599455B
Patent No. 5972621
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,455B
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/017001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-599-455B-2

Query Match 76.7%; Score 3345; DB 2; Length 894;
Best Local Similarity 76.0%; Pred. No. 3.6e-298;
Matches 609; Conservative 73; Mismatches 117; Indels 2; Caps 2;

QY 1 MICOKFCVLLHWEFIYVITAFNLSYPTWREKLSGPPNPNSTYDVFLLPAGLSKNTSNS 60
Db 1 MNCQKFVLLHWEFLYVIAALNAYLPISPWKEFLCGPPNTDDSFSLFAGAPNNSAL 60

QY 61 NGHYETAVERKFNSSGTHFNLSKTTFTHCCFRSEQDRNCSLCADNIEGRTFVSTVNSLVF 120
Db 61 KGASEAIVEAKFNSSGGIYVPELSKTVFHCCFGNEQGNCSALTNDTEGKTLASVVKASVF 120

QY 121 QQIDANNIQCWLKGDGLKLFICYVESLFPKLNPNYKVVHLLYVLEPEVLEDSPLVPQKGS 180
Db 121 ROLGVNWDIECHWKGDLTFLFICHEPLPRNPFKNYDSKVHLLYDLEPEVLEDSPLVPKDS 180

QY 181 FOMVHCNCSVHECCCLVPVPTAKLMDTLMLCLKITSGGVIFQSPPLMSVQPINMVKPDP 240
Db 181 FOTVOCNCSLRG-CECHVPVPRAKLYALLMVLLEITSAGVSFQSPPLMSLOPMLYKVPDP 239

QY 241 LGLHMEITDDGNLKISWSSPPLVPPLOQVQYKSENSTTVIREADKIVSATSLVDVSLP 300
Db 240 LGLHMEVTDGDNLKISWDSQTMAPPLOQVQYKLENS-TIVREAAEIVSATSLVDVSLP 298

QY 301 GSSYEYQVGRKLDGPGIWSMDSTPRVFTQDVIYFPFKILTSGVSNVSEFHCITYKKEKI 360
Db 299 GSSYEYQVGRKLDGSGVMSDSSPOVFTQDVIYFPFKILTSGVSNVSEFHCITYKKEKI 358

QY 361 VPSKEIVVMNLAEKIPQSDYVSDHVSQVTFNLTNETKPRGFTYDQVYCCNEHECHH 420
Db 359 TSSKQIVVMNLAEKIPQSDYVSDHVSQVTFNLTNETKPRGFTYDQVYCCNEHECHH 418

QY 421 RYAEIYVIVDININISCEITDGYLTMTCTCSTQSLAESLTQLRYHRSLSYCDSPSIH 480
Db 419 RYAEIYVIVDININISCEITDGYLTMTCTCSTQSLAESLTQLRYHRSLSYCDSPSIH 478

QY 481 PISEPKCYLQSDGFEYECIFQIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
Db 479 PTSEPKNCVLRQDGFYECVFPQIFLLSGYTMWIRINHSGLSDSPPTCVLPDSVVKPLPP 538

QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSKEVQWKMVEYDQAKSVSLPV 600
Db 539 SNVKAETVNTGLKVSWEKVPFPENNLOFQIRYGLSKEVQWKMVEYDQAKSVSLPV 598

QY 601 PDLCAVYAVQVRCRDLGLGYWSNMSNPAYTVVMDIKVPMRGPPEWRLINGDTMKKEKNV 660
Db 599 SDCAVYVQVRCRDLGLGYWSNMSNPAYTVVMDIKVPMRGPPEWRLINGDTMKKEKNV 658

QY 661 TLLMKPLMKNDSLCSVQRYVINHTSCNGTWSVEDYGNHTKFTFLWTEQAHVTVLAINSI 720
Db 659 TLLMKPLTKNDSLCSVRRYVVKHRTAHNGTWSVEDYGNHTKFTFLWTEQAHVTVLAINSI 718

QY 721 GASVANENLTFSPWMSKVNIVQSLAYSAYPLNSCVIVSWILSPSDYKLMFYIEWKNLNE 780
Db 719 GASLVNENLTFSPWMSKVSAYESLSAVPLSSCVLSWTLSPDDYSLLYLVIEWKILNED 778

QY 781 GEIKWLRISSSVKYYTHGKF 801
Db 779 DGMKWLRIPSNVKFFYHDNF 799

Search completed: October 22, 2001, 16:05:22
Job time: 92 sec

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THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 22, 2001, 16:05:01 ; Search time 31.06 Seconds

(without alignments)
3424.766 Million cell updates/sec

Title: US-09-116-676-10

Perfect score: 4363

Sequence: 1 MICQKFCVLLHWEFIYVIT.....WLRISSSVKYIYHCKFTIL 804

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_16:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_unclassified:*
- 13: sp_vertebrate:*
- 14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4337	99.4	896	Q92919	Q92919 homo sapien
2	4337	99.4	958	Q92920	Q92920 homo sapien
3	4337	99.4	1165	Q92921	Q92921 homo sapien
4	4325	99.1	896	Q13594	Q13594 homo sapien
5	4325	99.1	906	Q13593	Q13593 homo sapien
6	4325	99.1	958	Q13592	Q13592 homo sapien
7	4125	94.5	894	Q9MYL1	Q9MYL1 macaca mula
8	4125	94.5	925	Q9MYK9	Q9MYK9 macaca mula
9	4125	94.5	1163	Q9MYL2	Q9MYL2 macaca mula
10	4125	94.5	1194	Q9MYL0	Q9MYL0 macaca mula
11	3711	85.1	848	Q9MYL0	Q9MYL0 macaca mula
12	3709	85.0	1165	Q9MYS2	Q9MYS2 sus scrofa
13	3340	76.6	1162	Q02671	Q02671 sus scrofa
14	3284	75.3	895	Q13593	Q13593 homo sapien
15	2105.5	48.3	1147	Q9DOK1	Q9DOK1 mus musculus
16	2096.5	48.1	1148	Q9DOK1	Q9DOK1 mus musculus
17	2024.5	46.4	1146	Q918V6	Q918V6 gallus galli
18	1089	25.0	246	Q35773	Q35773 rattus norv
19	683	15.7	161	Q28606	Q28606 ovis aries

20	616	14.1	147	6	Q95257	Q95257 sus scrofa
21	497	11.4	123	6	Q9N1F9	Q9N1F9 sus scrofa
22	477	10.9	121	6	O18980	O18980 bos taurus
23	456	10.5	145	13	Q9IA32	Q9IA32 gallus galli
24	377.5	8.7	881	13	Q57519	Q57519 xenopus lae
25	313.5	7.2	918	13	Q9W6U9	Q9W6U9 gallus galli
26	299	6.9	57	6	O97778	O97778 elephas max
27	299	6.9	57	6	O97778	O97778 loxodonta a
28	279	6.4	710	13	O57520	O57520 xenopus lae
29	242.5	5.6	1093	11	O70535	O70535 rattus norv
30	220	5.0	2302	11	O88488	O88488 rattus norv
31	212.5	4.9	379	4	Q98650	Q98650 homo sapien
32	196.5	4.5	970	11	O88821	O88821 mus musculus
33	192	4.4	971	11	O70458	O70458 mus musculus
34	188	4.3	329	4	Q9UQ41	Q9UQ41 homo sapien
35	178	4.1	422	4	O75462	O75462 homo sapien
36	174	4.0	422	4	Q9UHH5	Q9UHH5 homo sapien
37	174.5	4.0	425	11	Q9JMS8	Q9JMS8 mus musculus
38	168.5	3.9	346	13	Q93404	Q93404 oreochromis
39	167.5	3.8	1598	4	Q9P214	Q9P214 homo sapien
40	166	3.8	1114	5	Q9VSG6	Q9VSG6 drosophila
41	163	3.7	6875	6	Q28733	Q28733 oryctolagus
42	162.5	3.7	2037	5	Q9VLS8	Q9VLS8 drosophila
43	161.5	3.7	26926	4	O10466	O10466 homo sapien
44	158.5	3.6	638	6	Q9XS21	Q9XS21 papio anubi
45	158	3.6	1005	13	P79921	P79921 xenopus lae

ALIGNMENTS

RESULT 1

Q92919 ID Q92919 PRELIMINARY; PRT: 896 AA.

AC Q92919; DT 01-FEB-1997 (Tremblrel. 02, Created)

DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)

DT -01-MAR-2001 (Tremblrel. 16, Last annotation update)

DE LEPTIN RECEPTOR.

GN DB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

[1]

RN SEQUENCE FROM N.A.

RP Bennett B.D., Solar G.P., Yuan J.O., Mathias J., Thomas G.R.,

RA Matthews W.; Curr. Biol. 6:0-0(0).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=97215244; PubMed=9061609;

RA Luoh S.M., Di Marco F., Levin N., Armanini M., Xie M.H., Nelson C.,

Bennett G.L., Williams M., Spencer S.A., Gurney A., de Sauvage F.J.;

"Cloning and characterization of a human leptin receptor using a

biologically active leptin immunoadhesin.";

J. Mol. Endocrinol. 18:77-85(1997).

DR EMBL; U66495; AAC07495.1;

DR EMBL; U50748; AAC23650.1;

DR HSSP; P40189; IBOU

DR InterPro; IPR001777;

DR InterPro; IPR002996;

DR InterPro; IPR003529;

DR InterPro; IPR003531;

DR Pfam; PF00041; fn3.2

DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.

DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.

DR SMART; SM00060; FN3; 1.

SQ SEQUENCE 896 AA; 102489 MW; D371C7A4186DEEF3 CRC64;

Query Match 99.4%; Score 4337; DB 4; Length 896;
Best Local Similarity 99.8%; Pred. No. 0;

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Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MICQKFCVLLHWEFIYVITAFNLSPYTPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
DB 1 MICQKFCVLLHWEFIYVITAFNLSPYTPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYETAPEKFNSSGTHFNSLKTTHFCCFSEODRNCSCADNIEGKTFVSTVNSLVF 120
DB 61 NGHYETAPEKFNSSGTHFNSLKTTHFCCFSEODRNCSCADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANNIQCWLKGLDLKLFICYVESLEFKNLFNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
DB 121 QOIDANNIQCWLKGLDLKLFICYVESLEFKNLFNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
QY 181 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCKLTSGGVIFQSPMSVQPINNVKPDPP 240
DB 181 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCKLTSGGVIFQSPMSVQPINNVKPDPP 240
QY 241 LGLHMEITDDGNLKIWSSSPLVPPELOVQYKYSNSTTVIREADKIVSATSLVDSILP 300
DB 241 LGLHMEITDDGNLKIWSSSPLVPPELOVQYKYSNSTTVIREADKIVSATSLVDSILP 300
QY 301 GSSYEVOVGRKRLDGPGLWSDSPPRVFTTQDVIYFPKILTSVGSNVSFHCIIYKKNKI 360
DB 301 GSSYEVOVGRKRLDGPGLWSDSPPRVFTTQDVIYFPKILTSVGSNVSFHCIIYKKNKI 360
QY 361 VPSKEIIVMMNLAEKIPQSOYDVVSDHVSQVTFNKLNETKPRGFTYDAVYCCNEHECHH 420
DB 361 VPSKEIIVMMNLAEKIPQSOYDVVSDHVSQVTFNKLNETKPRGFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNIINISCTDGYLTMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSII 480
DB 421 RYAEIYVIDVNIINISCTDGYLTMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSII 480
QY 481 PISEPKDCYQSDGFYECIFQPIFLLSGYTMWIRINISGLSDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYQSDGFYECIFQPIFLLSGYTMWIRINISGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKVPFENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLLKISWEKVPFENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
QY 601 PDLCAVAVQVRCRDLGLGYSWNSNPAYTVVMDIKVPMRGPEFNRINGDTMKKEKNV 660
DB 601 PDLCAVAVQVRCRDLGLGYSWNSNPAYTVVMDIKVPMRGPEFNRINGDTMKKEKNV 660
QY 661 TLLWPKLKNDSLCSVQRYVINHHTSCNGTWSDEVGNHKTFTLWTEQAHTVTVLAINSI 720
DB 661 TLLWPKLKNDSLCSVQRYVINHHTSCNGTWSDEVGNHKTFTLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEMKLNED 780
DB 721 GASVANFNLTFSWPMKSNVIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEMKLNED 780
QY 781 GEIKWLRISSVKKYYIHGKF 801
DB 781 GEIKWLRISSVKKYYIHGKF 801
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RESULT 2

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Q92920 PRELIMINARY; PRT; 958 AA.
ID Q92920
AC Q92920;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE LEPTIN RECEPTOR.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
```

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RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
RA Matthews W.;
RL Curr. Biol. 6:0-0(0).
DR EMBL: U66496; AB07496.1;
DR HSSP: P16471; 1BP3.
DR InterPro: IPR001777;
DR InterPro: IPR002996;
DR InterPro: IPR003529;
DR InterPro: IPR003531;
DR Pfam: PF00041; fn3.2.
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01353; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
SQ SEQUENCE 958 AA; 109392 MW; 3F65BC5A187E803A CRC64;
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Query Match 99.48; Score 4337; DB 4; Length 958;
Best Local Similarity 99.88; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 MICQKFCVLLHWEFIYVITAFNLSPYTPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
DB 1 MICQKFCVLLHWEFIYVITAFNLSPYTPWRFKLSMPPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHYETAPEKFNSSGTHFNSLKTTHFCCFSEODRNCSCADNIEGKTFVSTVNSLVF 120
DB 61 NGHYETAPEKFNSSGTHFNSLKTTHFCCFSEODRNCSCADNIEGKTFVSTVNSLVF 120
QY 121 QOIDANNIQCWLKGLDLKLFICYVESLEFKNLFNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
DB 121 QOIDANNIQCWLKGLDLKLFICYVESLEFKNLFNRYNYKVHLLYVLPVLEDSPLVPQKGS 180
QY 181 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCKLTSGGVIFQSPMSVQPINNVKPDPP 240
DB 181 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCKLTSGGVIFQSPMSVQPINNVKPDPP 240
QY 241 LGLHMEITDDGNLKIWSSSPLVPPELOVQYKYSNSTTVIREADKIVSATSLVDSILP 300
DB 241 LGLHMEITDDGNLKIWSSSPLVPPELOVQYKYSNSTTVIREADKIVSATSLVDSILP 300
QY 301 GSSYEVOVGRKRLDGPGLWSDSPPRVFTTQDVIYFPKILTSVGSNVSFHCIIYKKNKI 360
DB 301 GSSYEVOVGRKRLDGPGLWSDSPPRVFTTQDVIYFPKILTSVGSNVSFHCIIYKKNKI 360
QY 361 VPSKEIIVMMNLAEKIPQSOYDVVSDHVSQVTFNKLNETKPRGFTYDAVYCCNEHECHH 420
DB 361 VPSKEIIVMMNLAEKIPQSOYDVVSDHVSQVTFNKLNETKPRGFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNIINISCTDGYLTMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSII 480
DB 421 RYAEIYVIDVNIINISCTDGYLTMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSII 480
QY 481 PISEPKDCYQSDGFYECIFQPIFLLSGYTMWIRINISGLSDSPPTCVLPDSVVKPLPP 540
DB 481 PISEPKDCYQSDGFYECIFQPIFLLSGYTMWIRINISGLSDSPPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKVPFENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLLKISWEKVPFENNLOFQIRYGLSGKEVQWKMEYVDAKSKSVSLPV 600
QY 601 PDLCAVAVQVRCRDLGLGYSWNSNPAYTVVMDIKVPMRGPEFNRINGDTMKKEKNV 660
DB 601 PDLCAVAVQVRCRDLGLGYSWNSNPAYTVVMDIKVPMRGPEFNRINGDTMKKEKNV 660
QY 661 TLLWPKLKNDSLCSVQRYVINHHTSCNGTWSDEVGNHKTFTLWTEQAHTVTVLAINSI 720
DB 661 TLLWPKLKNDSLCSVQRYVINHHTSCNGTWSDEVGNHKTFTLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEMKLNED 780
DB 721 GASVANFNLTFSWPMKSNVIVQSLAYPLNSSCVIVSWILSPSDYKLMYFIIEMKLNED 780
QY 781 GEIKWLRISSVKKYYIHGKF 801
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Db 781 GEIKWLRISSVKKYIHDF 801
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RESULT 3
Q92921 ID Q92921 PRELIMINARY; PRT; 1165 AA.
AC Q92921:
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE LEPTIN RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bennett B.D., Solar G.P., Yuan J.Q., Mathias J., Thomas G.R.,
RA Matthews W.;
RL Curr. Biol. 6:0-0(0).
DR EMBL; U68497; AAB07497.1; -.
DR HSSP; P40189; IBQU.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003529; -.
DR InterPro; IPR003531; -.
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 1165 AA; 132493 MW; CAA03BEAF2602D0A CRC64;

Query Match 99.4%; Score 4337; DB 4; Length 1165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEIYVITAFNLSPYIPTRWFKLSCMPNSTDYDFLLPAGLSKNTS 60
Db 1 MICQKFCVLLHWEIYVITAFNLSPYIPTRWFKLSCMPNSTDYDFLLPAGLSKNTS 60
|||||
QY 61 NGHYETAVEPKFNSSGTHFSNLKSTTFHCCFRSEODRNSCLADNIEGKTFVTSNLSV 120
Db 61 NGHYETAVEPKFNSSGTHFSNLKSTTFHCCFRSEODRNSCLADNIEGKTFVTSNLSV 120
|||||
QY 121 QQIDANWNIQCKLGDGLFCYVESLFLKFNLFNRYNRYKHLLYVLPVLEDSPLVPQKGS 180
Db 121 QQIDANWNIQCKLGDGLFCYVESLFLKFNLFNRYNRYKHLLYVLPVLEDSPLVPQKGS 180
|||||
QY 181 FQVHCNCSVHCCBCLVPVPTAKLNDTLMLCKLITSGGVIFQSPMLSVQPINVKPDP 240
Db 181 FQVHCNCSVHCCBCLVPVPTAKLNDTLMLCKLITSGGVIFQSPMLSVQPINVKPDP 240
|||||
QY 241 LGLHMEITDGNLKSWSPPPLVPVLPQYQVYKSENSTTVIREADKIYVTSLLVDSILP 300
Db 241 LGLHMEITDGNLKSWSPPPLVPVLPQYQVYKSENSTTVIREADKIYVTSLLVDSILP 300
|||||
QY 301 GSSYEVQVGRKLDGPGIWSDMSTPRVFTQDVYFPPKILTSVGSNYSFHCYKKNKI 360
Db 301 GSSYEVQVGRKLDGPGIWSDMSTPRVFTQDVYFPPKILTSVGSNYSFHCYKKNKI 360
|||||
QY 361 VPSKEIWMNNAEKIPQSDYDWDHVSQVTFNNLNETKPKGFTYDAVYCCNEHECHH 420
Db 361 VPSKEIWMNNAEKIPQSDYDWDHVSQVTFNNLNETKPKGFTYDAVYCCNEHECHH 420
|||||
QY 421 RYAEIYVDVNIINISCTDGYLTMTCTRWSTSTIQSLAESTLQRLYHRSLSYCSIPSIH 480
Db 421 RYAEIYVDVNIINISCTDGYLTMTCTRWSTSTIQSLAESTLQRLYHRSLSYCSIPSIH 480
|||||
QY 481 PTSEPKDCYLOSDGFECIFQPIELLGTYMTWIRNHSIGSLDSPTCVLPDSVVKPLPP 540
Db 481 PTSEPKDCYLOSDGFECIFQPIELLGTYMTWIRNHSIGSLDSPTCVLPDSVVKPLPP 540
|||||

QY 541 SSVKAEITINIGLLKISWEKPPENNLOFQIRYGLSGKEVQWKMYEYVDASKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPPENNLOFQIRYGLSGKEVQWKMYEYVDASKSVSLPV 600
|||||
QY 601 PDLCAVAVQVCRKLDGLGYNSNPNATVYVMDIKVPMRGPEFWRIINGDPMKKEKNV 660
Db 601 PDLCAVAVQVCRKLDGLGYNSNPNATVYVMDIKVPMRGPEFWRIINGDPMKKEKNV 660
|||||
QY 661 TLLWKPLMKNDLSQVQRYVINHTSCNGTWSVDGNHKTFTFLMTEQAHVTVLAINSI 720
Db 661 TLLWKPLMKNDLSQVQRYVINHTSCNGTWSVDGNHKTFTFLMTEQAHVTVLAINSI 720
|||||
QY 721 GASVANFNLTFSWPMKSNVIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLND 780
Db 721 GASVANFNLTFSWPMKSNVIVOSLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLND 780
|||||
QY 781 GEIKWLRISSVKKYIHGKF 801
Db 781 GEIKWLRISSVKKYIHDF 801
|||||

RESULT 4
Q13594 ID Q13594 PRELIMINARY; PRT; 896 AA.
AC Q13594:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE B219/OB RECEPTOR ISOFORM HUB219.3 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cioffi J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
RA Platika D., Shodgrass H.R.;
RT "Novel B219/OB receptor isoforms: possible role of leptin in
RT hematopoiesis and reproduction.";
RL Nat. Med. 2:585-589(1996).
DR EMBL; U52914; AAC50511.1; -.
DR HSSP; P40189; IBQU.
DR InterPro; IPR001777; -.
DR InterPro; IPR002996; -.
DR InterPro; IPR003529; -.
DR InterPro; IPR003531; -.
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 896 B219/OB RECEPTOR ISOFORM HUB219.3.
SQ SEQUENCE 896 AA; 102515 MW; 73C431F8C578CD07 CRC64;

Query Match 99.1%; Score 4325; DB 4; Length 896;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEIYVITAFNLSPYIPTRWFKLSCMPNSTDYDFLLPAGLSKNTS 60
Db 1 MICQKFCVLLHWEIYVITAFNLSPYIPTRWFKLSCMPNSTDYDFLLPAGLSKNTS 60
|||||
QY 61 NGHYETAVEPKFNSSGTHFSNLKSTTFHCCFRSEODRNSCLADNIEGKTFVTSNLSV 120
Db 61 NGHYETAVEPKFNSSGTHFSNLKSTTFHCCFRSEODRNSCLADNIEGKTFVTSNLSV 120
|||||
QY 121 QQIDANWNIQCKLGDGLFCYVESLFLKFNLFNRYNRYKHLLYVLPVLEDSPLVPQKGS 180
Db 121 QQIDANWNIQCKLGDGLFCYVESLFLKFNLFNRYNRYKHLLYVLPVLEDSPLVPQKGS 180
|||||

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Db 121 QQIDANNWNIQWLGDKLFCYVESLFRKLNFRNYKVVHLLVYLPEVLEDSPLVPQKGS 180
QY 181 FQVHNCNSVHECCBCLVPVPTAKLNDTLMLCLKITSGGVIFQSPPLMSVQPINNVKPDPP 240
Db 181 FQVHNCNSVHECCBCLVPVPTAKLNDTLMLCLKITSGGVIFQSPPLMSVQPINNVKPDPP 240
QY 241 LGLHMEITDDGNLKIWSWSPPLVPFPLOVQVYKYSNSTVIREADKIYSATSLVDSILP 300
Db 241 LGLHMEITDDGNLKIWSWSPPLVPFPLOVQVYKYSNSTVIREADKIYSATSLVDSILP 300
QY 301 GSSYEYQVGRKLDGPGIWSWSPPLVPFPLOVQVYKYSNSTVIREADKIYSATSLVDSILP 360
Db 301 GSSYEYQVGRKLDGPGIWSWSPPLVPFPLOVQVYKYSNSTVIREADKIYSATSLVDSILP 360
QY 361 VPSKEIYVWNNLAEKIPQSOYQVDSVHVSQVTFNNLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIYVWNNLAEKIPQSOYQVDSVHVSQVTFNNLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNIINISCTDGYLTMTKCRWSTSTIOSLAESTLQRYHRSLSYCSIPSIH 480
Db 421 RYAEIYVIDVNIINISCTDGYLTMTKCRWSTSTIOSLAESTLQRYHRSLSYCSIPSIH 480
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCRDLGLGYSWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCRDLGLGYSWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWPKLKNDSLSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWPKLKNDSLSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVIVQSLSAYPLNSSCVIVSWILSPSDYKLMFYIEWKNLNED 780
Db 721 GASVANFNLTFSWPMKSNVIVQSLSAYPLNSSCVIVSWILSPSDYKLMFYIEWKNLNED 780
QY 781 GEIKWLRISSSVKRYIYHGRF 801
Db 781 GEIKWLRISSSVKRYIYHDF 801
```

RESULT 5

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Q13593 ID Q13593 PRELIMINARY; PRT; 906 AA.
AC Q13593
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
OS B219/OB RECEPTOR ISOFORM HUB219.2 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96206286; PubMed=8616721;
RA Clöff J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
RA Platika D., Snodgrass H.R.;
RT *Novel B219/OB receptor isoforms: possible role of leptin in
RT hematopoiesis and reproduction.*;
RL Nat. Med. 2:585-589(1996).
DR EMBL; U52913; RAC50510.1;
DR HSSP; P40189; 1BQU.
DR InterPro; IPR001777;
DR InterPro; IPR002996;
DR InterPro; IPR003529;
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RESULT 6

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DR InterPro; IPR003531;
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01353; HEMATOPO_REC_L_P2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
KW Signal.
FT CHAIN 1 21 POTENTIAL.
FT CHAIN 22 906 B219/OB RECEPTOR ISOFORM HUB219.2.
SQ SEQUENCE 906 AA; 103487 MW; 6D51126P3076626 CRC64;
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Query Match 99.1%; Score 4325; DB 4; Length 906;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MICQKFCVLLHWEIYVITAFNLSPYTPWRFKLSCHPPNSTYDYFLLPAGLSKNTSNS 60
Db 1 MICQKFCVLLHWEIYVITAFNLSPYTPWRFKLSCHPPNSTYDYFLLPAGLSKNTSNS 60
QY 61 NGHETAVEPEKFNSSGTHFSNLSTKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHETAVEPEKFNSSGTHFSNLSTKTFHCCFRSEODRNCSLCADNIEGKTFVSTVNSLVF 120
QY 121 QQIDANNWNIQWLGDKLFCYVESLFRKLNFRNYKVVHLLVYLPEVLEDSPLVPQKGS 180
Db 121 QQIDANNWNIQWLGDKLFCYVESLFRKLNFRNYKVVHLLVYLPEVLEDSPLVPQKGS 180
QY 181 FQVHNCNSVHECCBCLVPVPTAKLNDTLMLCLKITSGGVIFQSPPLMSVQPINNVKPDPP 240
Db 181 FQVHNCNSVHECCBCLVPVPTAKLNDTLMLCLKITSGGVIFQSPPLMSVQPINNVKPDPP 240
QY 241 LGLHMEITDDGNLKIWSWSPPLVPFPLOVQVYKYSNSTVIREADKIYSATSLVDSILP 300
Db 241 LGLHMEITDDGNLKIWSWSPPLVPFPLOVQVYKYSNSTVIREADKIYSATSLVDSILP 300
QY 301 GSSYEYQVGRKLDGPGIWSWSPPLVPFPLOVQVYKYSNSTVIREADKIYSATSLVDSILP 360
Db 301 GSSYEYQVGRKLDGPGIWSWSPPLVPFPLOVQVYKYSNSTVIREADKIYSATSLVDSILP 360
QY 361 VPSKEIYVWNNLAEKIPQSOYQVDSVHVSQVTFNNLNETKPRGKFTYDAVYCCNEHECHH 420
Db 361 VPSKEIYVWNNLAEKIPQSOYQVDSVHVSQVTFNNLNETKPRGKFTYDAVYCCNEHECHH 420
QY 421 RYAEIYVIDVNIINISCTDGYLTMTKCRWSTSTIOSLAESTLQRYHRSLSYCSIPSIH 480
Db 421 RYAEIYVIDVNIINISCTDGYLTMTKCRWSTSTIOSLAESTLQRYHRSLSYCSIPSIH 480
QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYLOSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPTCVLPDSVVKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 600
QY 601 PDLCAVYAVQVRCRDLGLGYSWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 PDLCAVYAVQVRCRDLGLGYSWNSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWPKLKNDSLSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
Db 661 TLLWPKLKNDSLSVQRYVINHHTSCNGTWSVDVGNHTKFTFLWTEQAHTVTVLAINSI 720
QY 721 GASVANFNLTFSWPMKSNVIVQSLSAYPLNSSCVIVSWILSPSDYKLMFYIEWKNLNED 780
Db 721 GASVANFNLTFSWPMKSNVIVQSLSAYPLNSSCVIVSWILSPSDYKLMFYIEWKNLNED 780
QY 781 GEIKWLRISSSVKRYIYHGRF 801
Db 781 GEIKWLRISSSVKRYIYHDF 801
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Q13592.
AC Q13592; PRELIMINARY; PRT; 958 AA.
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE B219/OB RECEPTOR ISOFORM HUB219.1 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=96206286; PubMed=8616721;
RA Cioffli J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A.,
RA Platika D., Snodgrass H.R.;
RT *Novel B219/OB receptor isoforms: possible role of leptin in
RT hematopoiesis and reproduction.*;
RL Nat. Med. 2:585-589(1996).
DR EMBL: U52912; AAC50509.1; -
DR HSP: P40189; IBOU.
DR InterPro: IPR001777; -
DR InterPro: IPR002996; -
DR InterPro: IPR003529; -
DR InterPro: IPR003531; -
DR Pfam: PF00041; fn3; 2
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
DR SIGNAL
FT CHAIN 1 21 POTENTIAL
FT CHAIN 22 958 B219/OB RECEPTOR ISOFORM HUB219.1.
SQ SEQUENCE 958 AA; 109418 MW; C7E0E8D18428677B CRC64;

Query Match 99.1%; Score 4325; DB 4; Length 958;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICOKFCVLLHWEFIVITAFNLSPITPWRKLSKMPNPNSTYDFLLPAGLSKNTNS 60
DB 1 MICOKFCVLLHWEFIVITAFNLSPITPWRKLSKMPNPNSTYDFLLPAGLSKNTNS 60
QY 61 NGHYETAPEKFNSSGTHFNSLTKTTHCCFRSEQRNCSLCADNIEGRTFVTSNLSVF 120
DB 61 NGHYETAPEKFNSSGTHFNSLTKTTHCCFRSEQRNCSLCADNIEGRTFVTSNLSVF 120
QY 121 QQIDANNIQCWLKGLDKLFCYVESLFLKFLFRNYKVKHLLVLPVLEDSPLVPQKGS 180
DB 121 QQIDANNIQCWLKGLDKLFCYVESLFLKFLFRNYKVKHLLVLPVLEDSPLVPQKGS 180
QY 181 FQMVHCNCSVHECCGLVPVPTAKLNDTLMLCKLITSGGVIFQSPMLSVQPINNVKPDPP 240
DB 181 FQMVHCNCSVHECCGLVPVPTAKLNDTLMLCKLITSGGVIFQSPMLSVQPINNVKPDPP 240
QY 241 LGLHMEITDGNLKIWSPPPLVPFLOQVQKYSNSTTVIREADKIVSATSLLDVSIPL 300
DB 241 LGLHMEITDGNLKIWSPPPLVPFLOQVQKYSNSTTVIREADKIVSATSLLDVSIPL 300
QY 301 GSSYEYQVGRKRLDGPGLNSDWSPTVFTODVYFPPKLTLSVGSNSVSHFCYKKNKI 360
DB 301 GSSYEYQVGRKRLDGPGLNSDWSPTVFTODVYFPPKLTLSVGSNSVSHFCYKKNKI 360
QY 361 VPSKEIWMNLAEPQSQDYVDSVSKVTFEFLNENETKPRGKFTYDAYCCNEHECHH 420
DB 361 VPSKEIWMNLAEPQSQDYVDSVSKVTFEFLNENETKPRGKFTYDAYCCNEHECHH 420
QY 421 RYAEIYVIVDWINISCTDGLYKMTCRWSTSTQSLAESTLQLRHRSLSYCDIPSIH 480
DB 421 RYAEIYVIVDWINISCTDGLYKMTCRWSTSTQSLAESTLQLRHRSLSYCDIPSIH 480
QY 481 PISEPKDCYLQSDGFECIFQPIFLLSGYTMWIRINHSLSGSDSPCTCVLPDVSVPKPLPP 540
DB 481 PISEPKDCYLQSDGFECIFQPIFLLSGYTMWIRINHSLSGSDSPCTCVLPDVSVPKPLPP 540
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
DB 541 SSVKAEITINIGLLKISWEKVPFPENNLOQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
QY 601 PDLCAVAVQVRKRLDGLGYWSNWPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 601 PDLCAVAVQVRKRLDGLGYWSNWPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
QY 661 TLLWKPLMKNDSLCSVORYVINHHSTSCNGTWSGDSVGNHTKFTFLATQEAHTVTVLAINSI 720
DB 661 TLLWKPLMKNDSLCSVORYVINHHSTSCNGTWSGDSVGNHTKFTFLATQEAHTVTVLAINSI 720
QY 721 GASVANFNLTFSMPMSKVNITVQSLISAYPLNSSCVIVSWILSPDYKLMYFIEMKNLNEED 780
DB 721 GASVANFNLTFSMPMSKVNITVQSLISAYPLNSSCVIVSWILSPDYKLMYFIEMKNLNEED 780
QY 781 GEIKWLRISSSVKYYIHGKF 801
DB 781 GEIKWLRISSSVKYYIHDF 801
RESULT 7
Q9MYL1 PRELIMINARY; PRT; 894 AA.
AC Q9MYL1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE LEPTIN RECEPTOR SHORT ISOFORM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE;
RX MEDLINE=98408931; PubMed=9738551;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RT *Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT expression in the adipose tissue of normal, hyperinsulinemic, and type
RT 2 diabetic rhesus monkeys.*;
RL Obes. Res. 6:353-360(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF225873; AAF35387.1; -
DR InterPro: IPR001777; -
DR InterPro: IPR002996; -
DR InterPro: IPR003529; -
DR InterPro: IPR003531; -
DR Pfam: PF00041; fn3; 2
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 894 AA; 102191 MW; B3CAF032238BAF9 CRC64;

Query Match 94.5%; Score 4125; DB 6; Length 894;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 762; Conservative 13; Mismatches 24; Indels 2; Gaps 1;

QY 1 MICOKFCVLLHWEFIVITAFNLSPITPWRKLSKMPNPNSTYDFLLPAGLSKNTNS 60
DB 1 MICOKFCVLLHWEFIVITAFNLSPITPWRKLSKMPNPNSTYDFLLPAGLSKNTNS 60
QY 61 NGHYETAPEKFNSSGTHFNSLTKTTHCCFRSEQRNCSLCADNIEGRTFVTSNLSVF 120
DB 61 NGHYETAPEKFNSSGTHFNSLTKTTHCCFRSEQRNCSLCADNIEGRTFVTSNLSVF 120
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Db 61 NGHYETAVE--FNSSDTHFSLNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSVF 118
QY 121 QOIDANWNIQCHLKGDLKLFICVYVSLFKNLFRNYKVVHLLYVLPEVLEDSPLVPQKGS 180
Db 119 QMGANWNIQCHLKGDLKLFICVYVSLFKNLFRNYKVVHLLYVLPEVLEDSPLVPQKGS 178
QY 181 FQMVHCNCSVHECCBLVPPVPTAKLNDTLMLCKLITSGGVIFOSPLMSVQPINNVKPDPP 240
Db 179 FQMVHCNCSVHECCBLVPPVPTAKLNDTLMLCKLITSGGVIFOSPLMSVQPINNVKPDPP 238
QY 241 LGLHMEITDDGNLKIWSWSPPLVPFPFLOQYKYSNSTVIRREADKIVSATSLLVDSILP 300
Db 239 LGLHMEITDDGNLKIWSWSPPLVPFPFLOQYKYSNSTVIRREADKIVSATSLLVDSILP 298
QY 301 GSSYEVQVGRKLDGPGIWSWSDSTPRVFTTQDVIYFPKILTSVGSNVSFHCIIYKKNKI 360
Db 299 GSSYEVQVGRKLDGPGIWSWSDSTPRVFTTQDVIYFPKILTSVGSNVSFHCIIYKKNKI 358
QY 361 VPSKEIWMNMNLAEKIPQSDYDVSQVSDHVSQVTFNENETKPRGKFTYDAVYCCNEHECHH 420
Db 359 VSSKKIWMNMNLAEKIPQSDYDVSQVSDHVSQVTFNENETKPRGKFTYDAVYCCNEHECHH 418
QY 421 RYAEIYVDVNIINISCEYDGYLTKMTCRWSTSTIOSLAESTLQRLYRHSLSLYCFDIPSIH 480
Db 419 RYAEIYVDVNIINISCEYDGYLTKMTCRWSTSTIOSLAESTLQRLYRHSLSLYCFDIPSIH 478
QY 481 PISEPKDCYLOSQDGYECIFOPFILLSGYTMWIRNHSIGSLDSDPTCVLPDSVVKPLPP 540
Db 479 PISEPKDCYLOSQDGYECIFOPFILLSGYTMWIRNHSIGSLDSDPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOQFIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 600
Db 539 SSVKAEITINIGLLKISWEKVPFPENNLOQFIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 598
QY 601 PDLCAVYAVQVCRKLDGPGIWSWSDSTPRVFTTQDVIYFPKILTSVGSNVSFHCIIYKKNKI 660
Db 599 PDLCAVYAVQVCRKLDGPGIWSWSDSTPRVFTTQDVIYFPKILTSVGSNVSFHCIIYKKNKI 658
QY 661 TLLWPKMKNESLCSVQRYVINHHSTSCNCTWSEDVGNHTKFTFLTEQAHTVTVLAINSI 720
Db 659 TLLWPKMKNESLCSVQRYVINHHSTSCNCTWSEDVGNHTKFTFLTEQAHTVTVLAINSI 718
QY 721 GASVANFNLTFSWPMKSNVIVQSLAYSAYPLNSCVITVSNILSPSDYKLMFYIEWKNLNED 780
Db 719 GASVANFNLTFSWPMKSNVIVQSLAYSAYPLNSCVITVSNILSPSDYKLMFYIEWKNLNED 778
QY 781 GEIKWLRISSSVKKYIIHDKF 801
Db 779 GEIKWLRISSSVKKYIIHDKF 799

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RESULT 8

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Q9MYK9 ID Q9MYK9 PRELIMINARY; PRT; 925 AA.
AC Q9MYK9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE LEPTIN RECEPTOR SHORT INSERT ISOFORM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE;
RX MEDLINE=98408931; PubMed=9738551;
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
expression in the adipose tissue of normal, hyperinsulinemic, and type
2 diabetic rhesus monkeys."

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RL Obes. Res. 6:353-360(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPOSE;
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Hansen B.C.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF225875; AAF35389.1;
DR InterPro: IPR001777;
DR InterPro: IPR002996;
DR InterPro: IPR003529;
DR InterPro: IPR003531;
DR Pfam: PF00041; fn3.2;
DR PROSITE: PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 925 AA; 105721 MW; EC09C27EC29C5F3A CRC64;

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Query Match 94.5%; Score 4125; DB 6; Length 925;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 762; Conservative 13; Mismatches 24; Indels 2; Gaps 1;

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QY 1 MICQKFCVLLHWEFIYITAFNLSPYITPWFKLSCHMPNSTYDYFLLPAGLSKNTNS 60
Db 1 MICQKFCVLLHWEFIYITAFNLSPYITPWFKLSCHMPNSTYDYFLLPAGLSKNTNS 60
QY 61 NGHYETAVEPKFNSSGTHFSNLKSTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSVF 120
Db 61 NGHYETAVE--FNSSDTHFSLNLSKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSVF 118
QY 121 QOIDANWNIQCHLKGDLKLFICVYVSLFKNLFRNYKVVHLLYVLPEVLEDSPLVPQKGS 180
Db 119 QMGANWNIQCHLKGDLKLFICVYVSLFKNLFRNYKVVHLLYVLPEVLEDSPLVPQKGS 178
QY 181 FQMVHCNCSVHECCBLVPPVPTAKLNDTLMLCKLITSGGVIFOSPLMSVQPINNVKPDPP 240
Db 179 FQMVHCNCSVHECCBLVPPVPTAKLNDTLMLCKLITSGGVIFOSPLMSVQPINNVKPDPP 238
QY 241 LGLHMEITDDGNLKIWSWSPPLVPFPFLOQYKYSNSTVIRREADKIVSATSLLVDSILP 300
Db 239 LGLHMEITDDGNLKIWSWSPPLVPFPFLOQYKYSNSTVIRREADKIVSATSLLVDSILP 298
QY 301 GSSYEVQVGRKLDGPGIWSWSDSTPRVFTTQDVIYFPKILTSVGSNVSFHCIIYKKNKI 360
Db 299 GSSYEVQVGRKLDGPGIWSWSDSTPRVFTTQDVIYFPKILTSVGSNVSFHCIIYKKNKI 358
QY 361 VPSKEIWMNMNLAEKIPQSDYDVSQVSDHVSQVTFNENETKPRGKFTYDAVYCCNEHECHH 420
Db 359 VSSKKIWMNMNLAEKIPQSDYDVSQVSDHVSQVTFNENETKPRGKFTYDAVYCCNEHECHH 418
QY 421 RYAEIYVDVNIINISCEYDGYLTKMTCRWSTSTIOSLAESTLQRLYRHSLSLYCFDIPSIH 480
Db 419 RYAEIYVDVNIINISCEYDGYLTKMTCRWSTSTIOSLAESTLQRLYRHSLSLYCFDIPSIH 478
QY 481 PISEPKDCYLOSQDGYECIFOPFILLSGYTMWIRNHSIGSLDSDPTCVLPDSVVKPLPP 540
Db 479 PISEPKDCYLOSQDGYECIFOPFILLSGYTMWIRNHSIGSLDSDPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOQFIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 600
Db 539 SSVKAEITINIGLLKISWEKVPFPENNLOQFIRYGLSGKEVQWKMYEYVDAKSKSVSLPV 598
QY 601 PDLCAVYAVQVCRKLDGPGIWSWSDSTPRVFTTQDVIYFPKILTSVGSNVSFHCIIYKKNKI 660
Db 599 PDLCAVYAVQVCRKLDGPGIWSWSDSTPRVFTTQDVIYFPKILTSVGSNVSFHCIIYKKNKI 658
QY 661 TLLWPKMKNESLCSVQRYVINHHSTSCNCTWSEDVGNHTKFTFLTEQAHTVTVLAINSI 720
Db 659 TLLWPKMKNESLCSVQRYVINHHSTSCNCTWSEDVGNHTKFTFLTEQAHTVTVLAINSI 718
QY 721 GASVANFNLTFSWPMKSNVIVQSLAYSAYPLNSCVITVSNILSPSDYKLMFYIEWKNLNED 780
Db 719 GASVANFNLTFSWPMKSNVIVQSLAYSAYPLNSCVITVSNILSPSDYKLMFYIEWKNLNED 778

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Db 719 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVILSMILSPDYKLMYFIIEWKLNLED 778
QY 781 GEIKWLRISSSVKKYIIRHGF 801
Db 779 GEIKWLRISSSVKKYIIRHGF 799
RESULT 9
Q9MYL2
ID Q9MYL2 PRELIMINARY; PRT; 1163 AA.
AC Q9MYL2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE LEPTIN RECEPTOR LONG FORM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE-98408931; PubMed-9738551;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT expression in the adipose tissue of normal, hyperinsulinemic, and type
RT 2 diabetic rhesus monkeys.";
RL Obes. Res. 6:353-360(1998).
RN [2]
RN SEQUENCE FROM N.A.
RA Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AF222960; AAF34683.1;
DR InterPro; IPR001777;
DR InterPro; IPR002996;
DR InterPro; IPR003529;
DR InterPro; IPR003531;
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
DR Receptor.
SQ SEQUENCE 1163 AA; 132295 MW; 6B7B89108F851895 CRC64;

Query Match 94.5%; Score 4125; DB 6; Length 1163;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 762; Conservative 13; Mismatches 24; Indels 2; Gaps 1;

QY 1 MICOKFCVLLHWEFIVITAFNLSYPTTPWRFKLSKMPNPNSTYDYELLPAGLSKNTSNS 60
Db 1 MICOKFCVLLHWEFIVITAFNLSYPTTPWRFKLSKMPNPNSTYDYELLPAGLSKNTS 60
QY 61 NGHETAVEPKFNSGTHFNLSKTTTHCCFRSQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHETAVE--FNSSDTHFNLSKTTTHCCFRSQDRNCSLCADNIEGKTFVSTVNSVF 118
QY 121 QQIDANNNIQCLWGLDKLFCYVESLFKNLFNRYKNVHLLVYLPVELESDPLVPQKGS 180
Db 119 QQGANNNIQCLWGLDKLFCYVESLFKNLFNRYKNVHLLVYLPVELESDPLVPQKGS 178
QY 181 FQVHNCVSHCECECLVPVPTAKLNDTLMLCLKITSGGVIFQSPMLSVOPINMKVPDP 240
Db 179 FQVHNCVSHCECECLVPVPTAKLNDTLMLCLKITSGGVIFQSPMLSVOPINMKVPDP 238
QY 241 LGLHMETDGNLKNISWSPPLVPFPFQYQVQKYSNSTTVIREADKIVSATSLIVDSILP 300
Db 239 LGLHMETDGNLKNISWSPPLVPFPFQYQVQKYSNSTTVIREADKIVSATSLIVDILP 298
QY 301 GSSYEYQVRKRLDGPGLWSDWSTPRVFTTQDVIYFPFKILTSGVSNVSHFYKKNKI 360
Db 299 GSSYEYQVRKRLDGPGLWSDWSTPRVFTTQDVIYFPFKILTSGVSNVSHFYKKNKI 358

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QY 361 VPSKEIVWMNLAEKIPQSDYVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 420
Db 359 VSSKIVWMNLAEKIPQSDYVSDHVSQVTFEFLNETKPRGKFTYDAVYCCNEHECHH 418
QY 421 RYAELYVIDVNIINISCEITDGYLTKMTKRWSTSTIQSLAEESTLQRLYHRSSLYCSDIPSIIH 480
Db 419 RYAELYVIDVNIINISCEITDGYLTKMTKRWSTSTIQSLAGSTLQRLYHRSSLYCSDIPSIIH 478
QY 481 PISEPKCYLQSDGYFECIFQPIELLSGYTWIRINHSGLSDSPPTCVLPDPSVVKPLPP 540
Db 479 PISEPKCYLQSDGYFECIFQPIELLSGYTWIRINHPGLSDSPPTCVLPDPSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKVPENNLOFOIRYCLSGKEVQWKMVEYDAKSYSVLPV 600
Db 539 SSVKAEITINIGLLKISWEKVPENNLOFOIRYCLSGKEIQWKMVDYDAKSYSVLPV 598
QY 601 PDLCAVAVQVRKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWIRINGDTMKKEKNV 660
Db 599 PDLCAVAVQVRKRLDGLGYWSNWSNPAYTVVMDIKVPMRGPEFWIRINGDTMKKEKNV 658
QY 661 TLLKPLMKNDLSCSVORYVINHTSCNGTWSVDGNHTKFTFLWTEQAHVTVVLAINSI 720
Db 659 TLLKPLMKNDLSCSVORYVINHTSCNGTWSVDGNHTKFTFLWTEQAHVTVVLAINSI 718
QY 721 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVILSMILSPDYKLMYFIIEWKLNLED 780
Db 719 GASVANFNLTFSWPMKVNIVQSLAYPLNSSCVILSMILSPDYKLMYFIIEWKLNLED 778
QY 781 GEIKWLRISSSVKKYIIRHGF 801
Db 779 GEIKWLRISSSVKKYIIRHGF 799

RESULT 10
Q9MYL2
ID Q9MYL2 PRELIMINARY; PRT; 1194 AA.
AC Q9MYL2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE LEPTIN RECEPTOR LONG INSERT ISOFORM.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RN SEQUENCE FROM N.A.
RX TISSUE-ADIPOSE;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RT "Monkey leptin receptor mRNA: sequence, tissue distribution, and mRNA
RT expression in the adipose tissue of normal, hyperinsulinemic, and type
RT 2 diabetic rhesus monkeys.";
RL Obes. Res. 6:353-360(1998).
RN [2]
RN SEQUENCE FROM N.A.
RX TISSUE-ADIPOSE;
RA Hotta K., Gustafson T.A., Ortmeyer H.K., Bodkin N.L., Hansen B.C.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AF225874; AAF35388.1;
DR InterPro; IPR001777;
DR InterPro; IPR002996;
DR InterPro; IPR003529;
DR InterPro; IPR003531;
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART; SM00060; FN3; 1.
DR Receptor.
SQ SEQUENCE 1194 AA; 135824 MW; 76D023E659911AA9 CRC64;

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Query Match      94.5%; Score 4125; DB 6; Length 1194;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 762; Conservative 13; Mismatches 24; Indels 2; Gaps 1;

QY 1 MICOKFCVLLHWEFIVITAFNLSPYDTPRRFKLSCLMPPNSTYDYFLLPAGLSKNTS 60
DB 1 MICOKFCVLLHWEFIVITAFNLSPYDTPRRFKLSCLMPPNSTYDYFLLPAGLSKNTS 60
QY 61 NGHYETAVERKFNSSGTHFSNLKTTFHCCFRSEQDRNCSLCADNTEGKTFVSTVNSLVF 120
DB 61 NGHYETAVERKFNSSGTHFSNLKTTFHCCFRSEQDRNCSLCADNTEGKTFVSTVNSLVF 118
QY 121 QOQDANNIOCLKGLDKLFCYVESLFKLNFRNYKVVHLLVYLPEVLEDSPLVPQKS 180
DB 119 QOQDANNIOCLKGLDKLFCYVESLFKLNFRNYKVVHLLVYLPEVLEDSPLVPQKS 178
QY 181 FOMVHCNCSVHECECLVPVPTAKLNDTLMLCKLITSGGVIFOSPLMSVQPINNVKPDPP 240
DB 179 FOMVHCNCSVHECECLVPVPTAKLNDTLMLCKLITSGGVIFOSPLMSVQPINNVKPDPP 238
QY 241 LGLHMETDDGNLKIWSPPPLVPFPLOQYKYSNSTTVIREADKIVSATSLVDSILP 300
DB 239 LGLHMETDDGNLKIWSPPPLVPFPLOQYKYSNSTTVIREADKIVSATSLVDSILP 298
QY 301 GSSYEVOVRKRLDGLGINSWSTPRVFTTQDVIYPPPKILTSVGNVSFHCYKKNKI 360
DB 299 GSSYEVOVRKRLDGLGINSWSTPRVFTTQDVIYPPPKILTSVGNVSFHCYKKNKI 358
QY 361 VPSKEIYVWNNLAELKIPQSOYDVSVHVSFNFNLNETKPKGKTFYDAVCCNEHECHH 420
DB 359 VPSKEIYVWNNLAELKIPQSOYDVSVHVSFNFNLNETKPKGKTFYDAVCCNEHECHH 418
QY 421 RYAEKVIVDNNISCTDGLTKMTCRWSTSTIOSLAESTLQRLYHRSLSLYCSDIPSIH 480
DB 419 RYAEKVIVDNNISCTDGLTKMTCRWSTSTIOSLAESTLQRLYHRSLSLYCSDIPSIH 478
QY 481 PISEPKDCYLOSDFECLFQPIFLLSGTWMIRINHSGLSDSPPTCVLPDSVVKPLPP 540
DB 479 PISEPKDCYLOSDFECLFQPIFLLSGTWMIRINHSGLSDSPPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWKPVPFPENNLOFQIRYGLSGKEVQKMYEYVDAKSKSVSLPV 600
DB 539 SSVKAEITINIGLLKISWKPVPFPENNLOFQIRYGLSGKEVQKMYEYVDAKSKSVSLPV 598
QY 601 PDLCAVAVQVRCKRLDGLGYSVNSNPAYTVVMDIKVPMRGPPEFWRINGDTMKKEKNV 660
DB 599 PDLCAVAVQVRCKRLDGLGYSVNSNPAYTVVMDIKVPMRGPPEFWRINGDTMKKEKNV 658
QY 661 TLLWPKLNKNSLCSVQRYVINHHTSCNWTSEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
DB 659 TLLWPKLNKNSLCSVQRYVINHHTSCNWTSEDVGNHTKFTFLWTEQAHTVTVLAINSI 718
QY 721 GASVANFNLTFSWPKSVKNIVOSLSAYPLNNSCVIVSWILSPDYKLMFYIENWNLND 780
DB 719 GASVANFNLTFSWPKSVKNIVOSLSAYPLNNSCVIVSWILSPDYKLMFYIENWNLND 778
QY 781 GEIKWLRISSVKKYIYHGKF 801
DB 779 GEIKWLRISSVKKYIYHDF 799

RESULT 11
ID Q9MZS2 PRELIMINARY; PRT; 848 AA.
AC Q9MZS2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TRANSMEMBRANE LEPTIN RECEPTOR (FRAGMENT).
OS OBR.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

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NCBI_TaxID=9823;
OX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=LIVER;
RC Hu X., Dai R., Li N., Wu C.;
RT *Expression, Detection, and Partial Cloning of Porcine Leptin Receptor
RT (OBR) Gene.*;
RL Submitted (JUL-1999) to the ENBL/GenBank/DBJ databases.
DR EMBL: AF167719, RAF89633.1;
DR InterPro: IPR001777;
DR InterPro: IPR002996;
DR InterPro: IPR003529;
DR InterPro: IPR003531;
DR Pfam: PF00041, fn3, 1;
DR PROSITE: PS01353; HEMATOPO_REC_L_P2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART: SM00060; FN3; 1.
KW Receptor.
FT NON_TER 1 848
FT SEQUENCE 848 AA; 96372 MW; 0C5AD3B40B278FAB CRC64;
SQ SEQUENCE 848 AA; 96372 MW; 0C5AD3B40B278FAB CRC64;

Query Match      85.1%; Score 3711; DB 6; Length 848;
Best Local Similarity 85.9%; Pred. No. 5e-300;
Matches 684; Conservative 40; Mismatches 70; Indels 2; Gaps 2;

QY 7 CVVLLHWEIYVITAFNLSPYDTPRRFKLSCLMPPNSTYDYFLLPAGLSKNTSNGHYET 66
DB 1 CVVLLHWEIYVITAFNLSPYDTPRRFKLSCLMPPNSTYDYFLLPAGLSKNTSNGHYET 59
QY 67 AVEPKNSSGTHFSNLKTTFHCCFRSEQDRNCSLCADNTEGKTFVSTVNSLVFQOQIDA 125
DB 60 VVEMELNSSGTHFSNLKTTFHCCFRSEQDRNCSLCADNTEGKTFVSTVNSLVFQOQIDA 119
QY 126 NNIOCLKGLDKLFCYVESLFKLNFRNYKVVHLLVYLPEVLEDSPLVPQKSQFQVH 185
DB 120 NNIOCLKGLDKLFCYVESLFKLNFRNYKVVHLLVYLPEVLEDSPLVPQKSQFQVH 179
QY 186 CNCVHCECECLVPVPTAKLNDTLMLCKLITSGGVIFOSPLMSVQPINNVKPDPLGLHM 245
DB 180 CNCVHCECECLVPVPTAKLNDTLMLCKLITSGGVIFOSPLMSVQPINNVKPDPLGLHM 239
QY 246 EITDDGNLKIWSPPPLVPFPLOQYKYSNSTTVIREADKIVSATSLVDSILPGSSYE 305
DB 240 EITDDGNLKIWSPPPLVPFPLOQYKYSNSTTVIREADKIVSATSLVDSILPGSSYE 299
QY 306 VQVRKRLDGLGINSWSTPRVFTTQDVIYPPPKILTSVGNVSFHCYKKNKIVPSKE 365
DB 300 VQVRKRLDGLGINSWSTPRVFTTQDVIYPPPKILTSVGNVSFHCYKKNKIVPSKE 359
QY 366 IYVWNNLAELKIPQSOYDVSVHVSFNFNLNETKPKGKTFYDAVCCNEHECHHRYAEL 425
DB 360 IYVWNNLAELKIPQSOYDVSVHVSFNFNLNETKPKGKTFYDAVCCNEHECHHRYAEL 419
QY 426 YVIDVNNISCTDGLTKMTCRWSTSTIOSLAESTLQRLYHRSLSLYCSDIPSIHPISEP 485
DB 420 YVIDVNNISCTDGLTKMTCRWSTSTIOSLAESTLQRLYHRSLSLYCSDIPSIHPISEP 479
QY 486 KDCYLQSDGFECLFQPIFLLSGTWMIRINHSGLSDSPPTCVLPDSVVKPLPPSSVKA 545
DB 480 KDCYLQSDGFECLFQPIFLLSGTWMIRINHSGLSDSPPTCVLPDSVVKPLPPSSVKA 539
QY 546 EITINIGLLKISWKPVPFPENNLOFQIRYGLSGKEVQKMYEYVDAKSKSVSLVPOLCA 605
DB 540 EITINIGLLKISWKPVPFPENNLOFQIRYGLSGKEVQKMYEYVDAKSKSVSLVPOLCA 599
QY 606 VYAVOVRCKRLDGLGYSVNSNPAYTVVMDIKVPMRGPPEFWRINGDTMKKEKNVTLWK 665
DB 600 VYAVOVRCKRLDGLGYSVNSNPAYTVVMDIKVPMRGPPEFWRINGDTMKKEKNVTLWK 659
QY 666 PLMKNDLSLCSVQRYVINHHTSCNWTSEDVGNHTKFTFLWTEQAHTVTVLAINSIGASVA 725
DB 666 PLMKNDLSLCSVQRYVINHHTSCNWTSEDVGNHTKFTFLWTEQAHTVTVLAINSIGASVA 725

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Db 660 PLMKNDLCSVRSYVVKHHTSRHGTWSDVGNHTKFLTLTEQAHSHVTVLAVNSIGASSA 719
Qy 726 NFNLTFSPMSKVNIVOSLSAYPLNSSCVIVSWLSPSKLMTYFIIEMKLNLEDGEIKW 785
Db 720 NFNLTFSPMSKVNIVOSLSAYPLNSSCVGLSWLSPSKLMTYFIIEMKLNLEDGEIKW 779
Qy 786 LRISSVKKYIHKCF 801
Db 780 LRISSVKKYIHDHF 795

RESULT 12
002671
ID 002671 PRELIMINARY; PRT; 1165 AA.
AC 002671;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE TRANSMEMBRANE LEPTIN RECEPTOR.
GN LEPR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Men T.Y., Lacroix D.A., Ruiz-Cortes Z.T., Song J.H., Palin M.-F.,
RA Murphy B.D.;
RT "Porcine leptin (Ob) receptor complete coding sequence.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 408-470 FROM N.A.
RX MEDLINE-97222487; PubMed-9069130;
RA Ernst C.W., Kapke P.A., Yerle M., Rothschild M.F.;
RT "The leptin receptor gene (LEPR) maps to porcine chromosome 6.";
RL Mamm. Genome 8:226-226(1997).
DR EMBL; AS092422; AAC61766.1;
DR EMBL; U72070; AAC48707.1;
DR HSSP; P16471; 1BP3.
DR InterPro; IPR001777;
DR InterPro; IPR002996;
DR InterPro; IPR003529;
DR InterPro; IPR003531;
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW Transmembrane.
SQ SEQUENCE 1165 AA; 132548 MW; 1BEB562FEA282F12 CRC64;

Query Match 85.0%; Score 3709; DB 6; Length 1165;
Best Local Similarity 85.3%; Pred. No. 1.1e-299;
Matches 684; Conservative 40; Mismatches 76; Indels 2; Gaps 2;

Qy 1 MLCQKFCVLLHFEFIVITAFNLSTPTTPWRKLSKMPNPNSTYDFLLPAGLSKNTSNS 60
Db 1 MTCPKFVALLHFEFIVITAFNLSTPTTPWRKLSKMPNPNSTYDFLLPAGLSKNTSTL 59
Qy 61 NGHYETAPEKPNSSGTHFNSL-SKTFHCFSRSEDRNCGLCADNIEGKTFVSTVNSLV 119
Db 60 NGHDEAVFETELNISTYISLNSKTFHCFSRSEDRNCGLCADNIEGKTFVSTVNSLV 119
Qy 120 FOQIDANNIQCWLKGLKFLICYVESLFRNRYNRYKVLHLYLVPEVLEDSPLVPQKG 179
Db 120 FOQTGANNNIQCWLKGLKFLICYMESLFRNRYNRYKVLHLYLVLEVLEGSPLLPQKG 179
Qy 180 SFQWVHCNCSVHECCCLVPVPVPAKLNLDLMLCKLTSGVIFQSPPLMSVQPINVYKPD 239
Db 180 SFQSVQNCNCSARECCCHVPVSAKLNLYLMLKLTSGVAFPHSPLMSVQPINVYKPD 239
Qy 240 PLGLHMEITDGNLKLWSWSPPLVPPLQYQVYKSENSTVIREADKIYSATSLLDVDSL 299

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Db 240 PLGLHMEITDGNLKLWSWSPPLVPPLQYQVYKSENSTVIREADKIYSATSLLDVDSL 299
Qy 300 PGSSYEVOVGRKLDGPGIWSDMSTPRVFTTQDVIYPPPKILTSVGSNVSFHCYKKNK 359
Db 300 PGSSYEVOVGRKLDGPGIWSDMSTPRVFTTQDVIYPPPKILTSVGSNVSFHCYKKNK 359
Qy 360 IVPSKEIYVWNNLAETIPQSOYDVVSDHVSQVTFNFIETKPRGKFTYDAYVCCNEHECH 419
Db 360 IVSSKIKIYVWNNLAETIPQSOYDVVSDHVSQVTFNFIETKPRGKFTYDAYVCCNEHECH 419
Qy 420 HRYAELVIVDNNINISCTDGYLTWKTCRSTSTIQSLAESTLQLRYHRSLSLCSYDPSI 479
Db 420 HRYAELVIVDNNINISCTDGYLTWKTCRSTSTIQSLAESTLQLRYHRSLSLCSYDPSI 479
Qy 480 HPISPKDCYLQSDGFEYECIFQPIFLISGYTMTIRINHSGLSDSPPTCVLPDSVYKPLP 539
Db 480 HPISPKDCYLQSDGFEYECIFQPIFLISGYTMTIRINHSGLSDSPPTCVLPDSVYKPLP 539
Qy 540 PSSVKAETITNIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKYEVYDTKLKSTSLP 599
Db 540 PSSVKAETITNIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKYEVYDTKLKSTSLP 599
Qy 600 VPDLCAVAYQVRCRKLGLDGLGYWSNMSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKN 659
Db 600 VPDLCAVAYQVRCRKLGLDGLGYWSNMSNPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKN 659
Qy 660 VTLWKPLMKNDLCSVRSYVVKHHTSRHGTWSDVGNHTKFLTLTEQAHSHVTVLAVNS 719
Db 660 VTLWKPLMKNDLCSVRSYVVKHHTSRHGTWSDVGNHTKFLTLTEQAHSHVTVLAVNS 719
Qy 720 IGASVANFLTFSPMSKVNIVOSLSAYPLNSSCVIVSWLSPSKLMTYFIIEMKLNLE 779
Db 720 IGASVANFLTFSPMSKVNIVOSLSAYPLNSSCVIVSWLSPSKLMTYFIIEMKLNLE 779
Qy 780 DGEIKWLRISSVKKYIHKCF 801
Db 780 DGEIKWLRISSVKKYIHDHF 801

RESULT 13
09QWG3
ID 09QWG3 PRELIMINARY; PRT; 1162 AA.
AC 09QWG3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE LEPTIN RECEPTOR B.
GN LEPRB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KK OBES; TISSUE=BRAIN, HYPOTHALAMUS;
RA Igel M., Taylor B.A., Phillips S.J., Becker W., Herberg L.,
RA Joost H.G.;
RT "Hyperleptinemia and leptin receptor variant Asp600Asn in the obese,
RT hyperinsulinemic KK mouse strain.";
RL J. Endocrinol. 21:337-345(1998).
DR EMBL; Y10296; CAA71342.1;
DR HSSP; P40189; 1BQU.
DR InterPro; IPR001777;
DR InterPro; IPR002996;
DR InterPro; IPR003529;
DR InterPro; IPR003531;
DR Pfam; PF00041; fn3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
KW SMART; SM00060; FN3; 1.
RECEPTOR.
FT VARIANT 600 600 N -> D.
SQ SEQUENCE 1162 AA; 130786 MW; 541E77CBB46EC00D CRC64;

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Query Match      76.6%; Score 3340; DB 11; Length 1162;
Best Local Similarity 75.9%; Pred. No. 5.6e-269;
Matches 608; Conservative 74; Mismatches 117; Indels 2; Gaps 2;

OC 1 MICQKFCVLLHWEFYIVITAFNLSPITPWRFKLSMPNPSTYDFLLPAGLSKNTS 60
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RA Wang M.Y., Unger R.H.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U53144; AAB03088.1;
DR HSP: P40189; IBOU.
DR InterPro: IPR001777;
DR InterPro: IPR002996;
DR InterPro: IPR003529;
DR InterPro: IPR003531;
DR Pfam: PF00041; fn3.2;
DR PROSITE: PS01353; HEMATOPO_REC_L_P2; UNKNOWN_1.
DR PROSITE: PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
DR SMART: SM00060; FN3.1.
SQ SEQUENCE 895 AA; 101324 MW; 3C93F018A737CC07 CRC64;

Query Match      75.3%; Score 3284; DB 11; Length 895;
Best Local Similarity 75.0%; Pred. No. 1.8e-264;
Matches 601; Conservative 77; Mismatches 121; Indels 2; Gaps 2;

QY 1 MICQKFCVLLHWEFYIVITAFNLSPITPWRFKLSMPNPSTYDFLLPAGLSKNTS 60
Db 1 MICQKFCVLLHWEFYIVITAFNLSPITPWRFKLSMPNPSTYDFLLPAGLSKNTS 60
QY 61 NGHYETAVEPKFNSSGTHFSNLKSTFFHCCFRSEQRNCSLCADNTEGKTEFVTSN 120
Db 61 NGHYETAVEPKFNSSGTHFSNLKSTFFHCCFRSEQRNCSLCADNTEGKTEFVTSN 120
QY 61 KGASEALVEAKFNSTGIYVSELSKTFHCCFEGNEQONCSALTGNTGKTLASVVKPL 120
Db 61 KGASEALVEAKFNSTGIYVSELSKTFHCCFEGNEQONCSALTGNTGKTLASVVKPL 120
QY 121 QOIDANNIQCWLKGLKLFICYVESLFNLFNRYNYKVHLLVYLVLEVDLSPLVPQKS 180
Db 121 QOIDANNIQCWLKGLKLFICYVESLFNLFNRYNYKVHLLVYLVLEVDLSPLVPQKS 180
QY 121 ROLGVNMDIECWKMGDLTLFICHMEPLPKNPKNYDSKVHLLYDLPEVIDDLPPLK 120
Db 121 ROLGVNMDIECWKMGDLTLFICHMEPLPKNPKNYDSKVHLLYDLPEVIDDLPPLK 120
QY 181 FQVHCNCSVHECCCLVPPVPTAKLNDTLMLCKITSGGVIFQSPMLSVQPINMKVPDP 240
Db 181 FQVHCNCSVHECCCLVPPVPTAKLNDTLMLCKITSGGVIFQSPMLSVQPINMKVPDP 240
QY 181 FQVHCNCSVRE-CECHVPPVPRAKNYALLMYLEITSAGVSFQSPMLSLQPMVVKPDP 239
Db 181 FQVHCNCSVRE-CECHVPPVPRAKNYALLMYLEITSAGVSFQSPMLSLQPMVVKPDP 239
QY 241 LGLHMEITDGNLKIWSPPPLVPFPLOVQYKSENSTTVIREADKIVSATSLVDSILP 300
Db 241 LGLHMEITDGNLKIWSPPPLVPFPLOVQYKSENSTTVIREADKIVSATSLVDSILP 300
QY 240 LGLRMEVTDGNLKIWSDSOTKAPFLQVQKYLENS-TIVREAAEIVSDTSLVDSVLP 298
Db 240 LGLRMEVTDGNLKIWSDSOTKAPFLQVQKYLENS-TIVREAAEIVSDTSLVDSVLP 298
QY 301 GSSYEYQVGRKRLDGPINSDMSTPRVFTQDVYPPPKILTSVGSNVSFHCYKKNKI 360
Db 301 GSSYEYQVGRKRLDGPINSDMSTPRVFTQDVYPPPKILTSVGSNVSFHCYKKNKI 360
QY 299 GSSYEYQVGRKRLDGPINSDMSTPRVFTQDVYPPPKILTSVGSNVSFHCYKKNKI 358
Db 299 GSSYEYQVGRKRLDGPINSDMSTPRVFTQDVYPPPKILTSVGSNVSFHCYKKNKI 358
QY 361 VPSKETIWMNLAELIPQSOYDVVSDHVSQVTFNINLNETKPRGKFTYDVCNNEHECH 420
Db 361 VPSKETIWMNLAELIPQSOYDVVSDHVSQVTFNINLNETKPRGKFTYDVCNNEHECH 420
QY 359 ISSKQIWMNLAELIPQSOYDVVSDHVSQVTFNINLNETKPRGKFTYDVCNNEHECH 418
Db 359 ISSKQIWMNLAELIPQSOYDVVSDHVSQVTFNINLNETKPRGKFTYDVCNNEHECH 418
QY 421 RYAEIVDVNINISCTDGYLTMTCTCRNSTSTIOSLAESTLQLRVHRSLSYCDIPSIH 480
Db 421 RYAEIVDVNINISCTDGYLTMTCTCRNSTSTIOSLAESTLQLRVHRSLSYCDIPSIH 480
QY 419 RYAEIVDVNINISCTDGYLTMTCTCRNSTSTIOSLAESTLQLRVHRSLSYCDIPSIH 478
Db 419 RYAEIVDVNINISCTDGYLTMTCTCRNSTSTIOSLAESTLQLRVHRSLSYCDIPSIH 478
QY 481 PISEPKDCYQSDGFEYCFQIFLGLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKDCYQSDGFEYCFQIFLGLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
QY 479 PISEPKDCYQSDGFEYCFQIFLGLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 538
Db 479 PISEPKDCYQSDGFEYCFQIFLGLSGYTMIRINHSLSGLSDSPPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMEYVDKSKVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMEYVDKSKVSLPV 600
QY 539 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMEYVDKSKVSLPV 598
Db 539 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMEYVDKSKVSLPV 598
QY 601 PDLCAVAVQVRCRDLGLGYNSNNSNPATVYVMDIKVPMRGPEFWRIINGDTMKKNY 660
Db 601 PDLCAVAVQVRCRDLGLGYNSNNSNPATVYVMDIKVPMRGPEFWRIINGDTMKKNY 660
QY 599 SDCAVYVQVRCRDLGLGYNSNNSNPATVYVMDIKVPMRGPEFWRIINGDTMKKNY 658
Db 599 SDCAVYVQVRCRDLGLGYNSNNSNPATVYVMDIKVPMRGPEFWRIINGDTMKKNY 658
QY 661 TLLWPKMKNDLSVQRYVYVNHHTSCNWTSEDVGNHHTKFTFLTEQARTVTVLAINSI 720
Db 661 TLLWPKMKNDLSVQRYVYVNHHTSCNWTSEDVGNHHTKFTFLTEQARTVTVLAINSI 720
QY 659 TLLWPKMKNDLSVQRYVYVNHHTSCNWTSEDVGNHHTKFTFLTEQARTVTVLAINSI 718
Db 659 TLLWPKMKNDLSVQRYVYVNHHTSCNWTSEDVGNHHTKFTFLTEQARTVTVLAINSI 718
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 22, 2001, 16:04:36 ; Search time 11.98 Seconds

(without alignments)
2298.949 Million cell updates/sec

Title: US-09-116-676-10

Perfect score: 4363

Sequence: 1 MICQKFCVLLHWEFIYVIT.....WLRISSVKYYIHGKFTIL 804

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4337	99.4	1165	1	LEPR_HUMAN
2	3345	76.7	1162	1	LEPR_MOUSE
3	3342	76.6	1162	1	LEPR_RAT
4	296	6.8	917	1	IL6B_MOUSE
5	277.5	6.4	918	1	IL6B_HUMAN
6	270.5	6.2	918	1	IL6B_RAT
7	246.5	5.6	837	1	GCSR_MOUSE
8	242.5	5.6	836	1	GCSR_HUMAN
9	221.5	5.1	1097	1	LIFR_HUMAN
10	208	4.8	1092	1	LIFR_MOUSE
11	205.5	4.7	874	1	IL2S_MOUSE
12	200.5	4.6	862	1	IL2S_HUMAN
13	181	4.1	831	1	PRLR_MELGA
14	178	4.1	831	1	PRLR_CHICK
15	166.5	3.8	2029	1	LAR_DROME
16	165	3.8	630	1	PRUR_ORENI
17	158.5	3.6	462	1	IL6A_RAT
18	157	3.6	830	1	PRLR_COLLI
19	153.5	3.5	460	1	IL6A_MOUSE
20	150.5	3.4	610	1	PRLR_RAT
21	147.5	3.4	638	1	GHR_MACMU
22	145	3.3	1493	1	NEOL_MOUSE
23	143	3.3	581	1	PRUR_CEREL
24	143	3.3	638	1	GHR_HUMAN
25	142.5	3.3	1461	1	NEOL_HUMAN
26	142	3.3	1447	1	DCC_HUMAN
27	141	3.2	581	1	PRUR_BOVIN
28	141	3.2	878	1	IL3B_MOUSE
29	140.5	3.2	638	1	GHR_PIG
30	140.5	3.2	638	1	GHR_RABIT
31	140	3.2	1377	1	NEOL_RAT
32	139	3.2	635	1	TPOR_HUMAN
33	136.5	3.1	1447	1	DCC_MOUSE

34	136.5	3.1	3063	1	CAIC_HUMAN	Q99715 homo sapien
35	135.5	3.1	1013	1	EPAS_CHICK	P54755 gallus gall
36	134.5	3.1	983	1	EPAS_MOUSE	P29319 mus musculus
37	134	3.1	362	1	CNTR_CHICK	P51641 gallus gall
38	134	3.1	608	1	PRLR_MOUSE	O08501 mus musculus
39	132.5	3.0	984	1	EPAS_RAT	O08680 rattus norv
40	132	3.0	1897	1	PTPF_HUMAN	P10566 homo sapien
41	132	3.0	2481	1	FINC_XENLA	P191740 xenopus lae
42	131.5	3.0	622	1	PRLR_HUMAN	P16471 homo sapien
43	131.5	3.0	634	1	GHR_BOVIN	P79108 bos taurus
44	131.5	3.0	634	1	GHR_SHEEP	Q28575 ovis aries
45	131.5	3.0	1443	1	NEOL_CHICK	Q90610 gallus gall

ALIGNMENTS

```
RESULT 1
LEPR_HUMAN
ID LEPR_HUMAN STANDARD; PRT; 1165 AA.
AC P48357;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LEPTIN RECEPTOR PRECURSOR (LEP-R) (OB RECEPTOR) (OB-R).
GN LEPR OR OBR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RC MEDLINE=96128129; PubMed=8548812;
RA Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,
RA Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J.,
RA Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,
RA Mays G.G., Wolf E.A., Monroe C.A., Tepper R.I.;
RT *Identification and expression cloning of a leptin receptor, OB-R.*;
RL Cell 83:1263-1271(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX Thompson D.B., Ossowski V., Sutherland J., Apel W.,
RA Biesterfeldt J.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP VARIANT ARG-223.
RX MEDLINE=96270489; PubMed=8666155;
RA Considine R.V., Considine E.L., Williams C.J., Hyde T.M., Caro J.F.;
RT *The hypothalamic leptin receptor in humans: identification of
RL fa/fa rat mutations.*;
RN [4]
RP Diabetes 45:992-994(1996).
RX VARIANTS ARG-109; ARG-204; ARG-223 AND ASN-656.
RX MEDLINE=97289527; PubMed=9144432;
RA Echwald S.M., Soerensen T.D., Soerensen T.I., Tybjaerg-Hansen A.,
RA Andersen T., Chung W.K., Leibel R.L., Pedersen O.;
RT *Amino acid variants in the human leptin receptor: lack of association
RL to juvenile onset obesity.*;
RN [5]
RP Biochem. Biophys. Res. Commun. 233:248-252(1997).
RX VARIANTS ARG-109; ARG-223 AND ASN-656.
RX MEDLINE=97431549; PubMed=9287054;
RA Chung W.K., Power-Kehoe L., Chua M., Chu F., Aronne L., Huma Z.,
RA Sothorn M., Udall J.N., Kahle B., Leibel R.L.;
RT *Exonic and intronic sequence variation in the human leptin receptor
RL gene (LEPR).*;
RN [6]
RP Diabetes 46:1509-1511(1997).
RX VARIANTS ARG-109 AND ARG-223.
RX MEDLINE=97301763; PubMed=9158141;
RA Thompson D.B., Ravussin E., Bennett P.H., Bogardus C.;
```

RT *Structure and sequence variation at the human leptin receptor gene in
lean and obese Pima Indians.*;
RN Hum. Mol. Genet. 6:675-679(1997).

RP VARIANTS ARG-109; ARG-223; ASN-656 AND THR-675.
RX MEDLINE=99075638; PubMed=9860295;

RA Roth H., Korn T., Rosenkranz K., Hinney A., Ziegler A., Kunz J.,
Siegfried W., Mayer H., Hebebrand J., Grzeschik K.-H.;

RT *Transmission disequilibrium and sequence variants at the leptin
receptor gene in extremely obese German children and adolescents.*;

RT Hum. Genet. 103:540-546(1998).

RL [8]

RN VARIANTS ARG-109; ARG-223 AND ASN-656.
RX MEDLINE=97318795; PubMed=9175732;

RA Gotoda T., Manning B.S., Goldstone A.P., Imrie H., Evans A.L.,
Strosberg A.D., McKelque P.M., Scott J., Altman T.J.;

RT *Leptin receptor gene variation and obesity: lack of association in a
white British male population.*;

RT Hum. Mol. Genet. 6:869-876(1997).

RL CC - FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC - SIMILARITY: CONTAINS 3 FIBROBLAST TYPE III-LIKE DOMAINS.

CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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CC EMBL; U43168; AAA93015.1; .

CC EMBL; U59263; AAB09673.1; JOINED.

CC EMBL; U59248; AAB09673.1; JOINED.

CC EMBL; U59249; AAB09673.1; JOINED.

CC EMBL; U59250; AAB09673.1; JOINED.

CC EMBL; U59251; AAB09673.1; JOINED.

CC EMBL; U59252; AAB09673.1; JOINED.

CC EMBL; U59253; AAB09673.1; JOINED.

CC EMBL; U59254; AAB09673.1; JOINED.

CC EMBL; U59255; AAB09673.1; JOINED.

CC EMBL; U59256; AAB09673.1; JOINED.

CC EMBL; U59257; AAB09673.1; JOINED.

CC EMBL; U59258; AAB09673.1; JOINED.

CC EMBL; U59259; AAB09673.1; JOINED.

CC EMBL; U59260; AAB09673.1; JOINED.

CC EMBL; U59261; AAB09673.1; JOINED.

CC EMBL; U59262; AAB09673.1; JOINED.

CC HSP; P10912; 3HHR.

CC MIM; 601007; .

CC InterPro; IPR001777; .

CC Pfam; PF00041; fn3.2.

CC PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.

CC Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism.

CC SIGNAL ?

CC CHAIN ?

CC DOMAIN ?

CC TRANSMEM 842 862

CC DOMAIN 863 1165

CC DOMAIN 237 320

CC DOMAIN 537 623

CC DOMAIN 738 823

CC CARBOHYD 23 23

CC CARBOHYD 41 41

CC CARBOHYD 56 56

CC CARBOHYD 73 73

CC CARBOHYD 81 81

CC CARBOHYD 98 98

CC CARBOHYD 187 187

CC CARBOHYD 206 206

CC CARBOHYD 276 276

CC CARBOHYD 347 347

FT	CARBOHYD	397	397	N-LINKED (GLCNAc)	(POTENTIAL)
FT	CARBOHYD	433	433	N-LINKED (GLCNAc)	(POTENTIAL)
FT	CARBOHYD	516	516	N-LINKED (GLCNAc)	(POTENTIAL)
FT	CARBOHYD	624	624	N-LINKED (GLCNAc)	(POTENTIAL)
FT	CARBOHYD	659	659	N-LINKED (GLCNAc)	(POTENTIAL)
FT	CARBOHYD	670	670	N-LINKED (GLCNAc)	(POTENTIAL)
FT	CARBOHYD	688	688	N-LINKED (GLCNAc)	(POTENTIAL)
FT	CARBOHYD	697	697	N-LINKED (GLCNAc)	(POTENTIAL)
FT	CARBOHYD	728	728	N-LINKED (GLCNAc)	(POTENTIAL)
FT	CARBOHYD	750	750	N-LINKED (GLCNAc)	(POTENTIAL)
FT	VARIANT	109	109	K -> R.	(POTENTIAL)
FT	VARIANT	204	204	/FTid=VAR_002703.	
FT	VARIANT	223	223	K -> R.	
FT	VARIANT	223	223	Q -> R.	
FT	VARIANT	656	656	/FTid=VAR_002705.	
FT	VARIANT	675	675	K -> N.	
FT	VARIANT	675	675	S -> T.	
FT	VARIANT	675	675	/FTid=VAR_002706.	
FT	VARIANT	675	675	/FTid=VAR_002707.	
SQ	SEQUENCE	1165 AA;	132449 MW;	8FF21D9AF5125808 CRC64;	

Query Match 99.4%; Score 4337; DB 1; Length 1165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MICQKFCVLLHWEFIYITAFNLSYPTTPWRFKLSCHMPNSTYDYFLPAGLSKNTNS 60
Db 1 MICQKFCVLLHWEFIYITAFNLSYPTTPWRFKLSCHMPNSTYDYFLPAGLSKNTNS 60

Qy 61 NGHETAVEPEFNSGTHFNSLSKTTTHCCFRSDRCNCLCADNIEGKTFVSTVNSLVF 120
Db 61 NGHETAVEPEFNSGTHFNSLSKTTTHCCFRSDRCNCLCADNIEGKTFVSTVNSLVF 120

Qy 121 QOIDANWNIQCLWGLDKLFCYVESLFKNLFNRYNRYKVHLLYVLPVLEDSPLVPQKGS 180
Db 121 QOIDANWNIQCLWGLDKLFCYVESLFKNLFNRYNRYKVHLLYVLPVLEDSPLVPQKGS 180

Qy 181 FQVHCNCSVHECCCLVPPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINVVKPDP 240
Db 181 FQVHCNCSVHECCCLVPPVPTAKLNDTLMLCLKITSGVIFQSPPLMSVQPINVVKPDP 240

Qy 241 LGLHMETDGCNLSKISSPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLVDSLTLP 300
Db 241 LGLHMETDGCNLSKISSPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLVDSLTLP 300

Qy 301 GSSYEVOVRGKRLDGPGLWSDWSTPRVFTTQDVIFPPPKILTSVGSNVSFHCYKKNKI 360
Db 301 GSSYEVOVRGKRLDGPGLWSDWSTPRVFTTQDVIFPPPKILTSVGSNVSFHCYKKNKI 360

Qy 361 VPSKEIYVWNNLAEKIPQSDVYSDVSHVSKVTBPNLNETPRGKFTYDQVYCCNHECHH 420
Db 361 VPSKEIYVWNNLAEKIPQSDVYSDVSHVSKVTBPNLNETPRGKFTYDQVYCCNHECHH 420

Qy 421 RYAEIYVDVNNINISCEGDTGLTKMTCTWSTSTIQSLAESTLQRYHRSSLYCSDIPSIH 480
Db 421 RYAEIYVDVNNINISCEGDTGLTKMTCTWSTSTIQSLAESTLQRYHRSSLYCSDIPSIH 480

Qy 481 PISEPKCYLQSDGDFYECIFQPIFLLSGYTNWIRINISLGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISEPKCYLQSDGDFYECIFQPIFLLSGYTNWIRINISLGLSDSPPTCVLPDSVVKPLPP 540

Qy 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
Db 541 SSVKAEITINIGLLKISWEKPVFPENNLFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600

Qy 601 PDLCAVAVQVRCRLDGLGWWSNPNATVYVMDIKVPMRGPPEFRIINGDTHMKKENV 660
Db 601 PDLCAVAVQVRCRLDGLGWWSNPNATVYVMDIKVPMRGPPEFRIINGDTHMKKENV 660

Qy 661 TLLWKLPMKNDLCSVQRYVINHHSTSCNGTWSEVDGHNHTFTFLWTQAAHTVTVLATNSI 720
Db 661 TLLWKLPMKNDLCSVQRYVINHHSTSCNGTWSEVDGHNHTFTFLWTQAAHTVTVLATNSI 720

Db 661 TLLMKPLMKNDLSCVQRYVINHHTSCNGTWSVDVGNHKTFTLWTRQAHVTVVLAINSI 720

Qy 721 GASVANFNLTSPKSKVNIQVLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
 |||||
 Db 721 GASVANFNLTSPKSKVNIQVLSAYPLNSSCVIVSWILSPSDYKLMYFIIEWKNLNED 780
 |||||

Qy 781 GEIKWLRISSSVKKYYIHGKF 801
 |||||
 Db 781 GEIKWLRISSSVKKYYIHDF 801

RESULT 2

ID LEPR_MOUSE STANDARD; PRT; 1162 AA.

AC P48356; O35686; Q61215; Q64309; O54986;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DE 30-MAY-2000 (Rel. 39, Last annotation update)

DE LEPTIN RECEPTOR PRECURSOR (LEP-R) (OB RECEPTOR) (OB-R) (B219 RECEPTOR).

GN LEP-R OR OB-R OR DB.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A. (VARIANT A).

RC TISSUE=Choroid plexus;

RX MEDLINE=96128129; PubMed=8548812;

RA Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J., Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds J., Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S., Mays G.G., Woolf E.A., Monroe C.A., Tepper R.I.;

RT "Identification and expression cloning of a leptin receptor, OB-R.";

RL Cell 83:1263-1271(1995).

RN [2]

RP SEQUENCE FROM N.A. (VARIANT B).

RC STRAIN=C57BL/KSJ; TISSUE=Hypothalamus;

RX MEDLINE=96190816; PubMed=8608603;

RA Chen H., Charlat O., Tartaglia L.A., Woolf E.A., Weng X., Ellis S.J., Lakey N.D., Culpepper J., Moore K.J., Breitbart R.E., Duyk G.M., Tepper R.I., Morgenstern J.P.;

RT "Evidence that the diabetes gene encodes the leptin receptor: identification of a mutation in the leptin receptor gene in db/db mice.";

RL Cell 84:491-495(1996).

RN [3]

RP SEQUENCE FROM N.A. (VARIANTS A TO E).

RC STRAIN=C57BL/KSJ; TISSUE=Hypothalamus;

RX MEDLINE=96231997; PubMed=86283397;

RA Lee G.-H., Proenca R., Montez J.M., Carroll K.M., Darvishzadeh J.G., Lee J.I., Friedman J.M.;

RT "Abnormal splicing of the leptin receptor in diabetic mice.";

RL Nature 379:632-635(1996).

RN [4]

RP SEQUENCE FROM N.A. (VARIANT C).

RC STRAIN=BALB/C; TISSUE=Liver;

RX MEDLINE=96206286; PubMed=8616721;

RA Clouff J.A., Shafer A.W., Zupancic T.J., Smith-Gbur J., Mikhail A., Platika D., Snodgrass H.R.;

RT "Novel B219/OB receptor isoforms: possible role of leptin in hematopoiesis and reproduction.";

RL Nat. Med. 2:585-589(1996).

RN [5]

RP SEQUENCE FROM N.A. (VARIANT B).

RC STRAIN=NEW ZEALAND OBESE / NZO; TISSUE=Hypothalamus;

RX MEDLINE=97462708; PubMed=9322935;

RA Igel M., Becker W., Herberg L., Joost H.G.;

RT "Hyperleptinemia, leptin resistance, and polymorphic leptin receptor in the New Zealand obese mouse.";

RL Endocrinology 138:4234-4239(1997).

RN [6]

RP SEQUENCE FROM N.A. (VARIANTS A AND B).

RC STRAIN=FVB/N; TISSUE=Spleen;

RX MEDLINE=96270520; PubMed=8692797;

RA Ghilardi N., Ziegler S., Wiestner A., Stoffel R., Heim M.H., Skoda R.C.;

RT "Defective STAT signaling by the leptin receptor in diabetic mice.";

RL Proc. Natl. Acad. Sci. U.S.A. 93:6231-6235(1996).

RN [7]

RP SEQUENCE FROM N.A. (VARIANT E).

RC STRAIN=129/J;

RX MEDLINE=98008913; PubMed=9344648;

RA Chua S.C., Koutas I.K., Han L., Liu S.M., Kay J., Young S.J., Chung W.K., Leibel R.L.;

RT "Fine structure of the murine leptin receptor gene: splice site suppression is required to form two alternatively spliced transcripts.";

RL Genomics 45:264-270(1997).

CC -1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).

CC -1- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT E) COULD FUNCTION AS A TRANSPORT PROTEIN.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E WHICH COULD BE SECRETED.

CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND E; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: (1) VARIANT A: HIGHEST LEVEL OF EXPRESSION IN LUNG AND KIDNEY, ALSO PRESENT IN CHOROID PLEXUS AND HYPOTHALAMUS. (2) VARIANT B: HIGHEST LEVEL OF EXPRESSION IN HYPOTHALAMUS AND LOWER LEVEL IN BRAIN, TESTES AND ADIPOSE TISSUE. (3) VARIANT E: EXPRESSED IN ADIPOSE TISSUE, HYPOTHALAMUS, HEART, AND TESTES.

CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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CC EMBL: U42467; AAA93014.1;

CC EMBL: U46135; AAC52408.1;

CC EMBL: U49106; AAC52420.1;

CC EMBL: U49107; AAC52421.1;

CC EMBL: U49108; AAC52422.1;

CC EMBL: U49109; AAC52423.1;

CC EMBL: U49110; AAC52424.1;

CC EMBL: U52915; AAC52599.1;

CC EMBL: Y10298; CAAY1343.1;

CC EMBL: U58861; AAC52705.1;

CC EMBL: U58862; AAC52706.1;

CC EMBL: U58863; AAC52707.1;

CC EMBL: AF039456; AAB95334.1;

CC EMBL: AF039443; AAB95334.1; JOINED.

CC EMBL: AF039444; AAB95334.1; JOINED.

CC EMBL: AF039445; AAB95334.1; JOINED.

CC EMBL: AF039446; AAB95334.1; JOINED.

CC EMBL: AF039447; AAB95334.1; JOINED.

CC EMBL: AF039448; AAB95334.1; JOINED.

CC EMBL: AF039449; AAB95334.1; JOINED.

CC EMBL: AF039450; AAB95334.1; JOINED.

CC EMBL: AF039451; AAB95334.1; JOINED.

CC EMBL: AF039452; AAB95334.1; JOINED.

CC EMBL: AF039453; AAB95334.1; JOINED.

CC EMBL: AF039454; AAB95334.1; JOINED.

CC EMBL: AF039455; AAB95334.1; JOINED.

CC HSP; P16471; IBP3.

CC MGD; MGI:104993; Lepr.

CC InterPro; IPR001777; -.

CC InterPro; IPR002465; -.

CC Pfam; PF00041; fn3; 3.

CC PROSITE; PS01353; HEMATOPO_REC_L_P2; 1.

CC Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;

KW

RA Karlsson C., Lindell K., Robinson I.C.A.F., Carlsson L.M.S.,
 RA Carlsson B.;
 RT *Cloning of the rat leptin receptor.*;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. AND VARIANT FA PRO-269 (VARIANT A).
 RC STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY;
 RX MEDLINE-96212906; PubMed-8630068;
 RA Iida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., Shima K.;
 RT *Phenotype-linked amino acid alteration in leptin receptor cDNA from
 RT Zucker fatty (fa/fa) rat.*;
 RL Biochem. Biophys. Res. Commun. 222:19-26(1996).
 RN [6]
 RP SEQUENCE OF 1-123 FROM N.A.
 RA Morishita T., Hidaka T., Kuzuyama T., Noguchi T.;
 RT *Analysis of rat leptin receptor gene.*;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE OF 694-878 FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Pancreas;
 RA Ma Z.;
 RT *Identification of a leptin receptor in islet.*;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE OF 843-892 FROM N.A. (VARIANT C).
 RC STRAIN-SPRAGUE-DAWLEY;
 RA Chien E.K., Hara M., Rouard M., Yano H., Philippe M., Polonsky K.S.,
 RA Bell G.I.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP VARIANT FA PRO-269.
 RX MEDLINE-96314329; PubMed-8690163;
 RA Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M., Okada N.,
 RA Kershaw E.E., Chung W.K., Power-Kehoe L., Chua M., Tartaglia L.A.,
 RA Leibel R.L.;
 RT *Phenotype of fatty due to Gln269Pro mutation in the leptin receptor
 RT (Lepr).*;
 RL Diabetes 45:1141-1143(1996).
 CC -1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).
 CC -1- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN
 CC TO THE CEREBROSPINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT
 CC E) COULD FUNCTION AS A TRANSPORT PROTEIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E
 CC WHICH COULD BE SECRETED.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND E;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- DISEASE: THE FATTY (FA) MUTATION PRODUCES PROFOUND OBESITY OF
 CC EARLY ONSET CAUSED BY HYPERPHAGIA, DEFECTIVE NONSHIVERING
 CC THERMOGENESIS, AND PREFERENTIAL DEPOSITION OF ENERGY INTO ADIPOSE
 CC TISSUE.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC
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 CC
 CC -----
 CC EMBL; U52966; AAC52587.1;
 CC EMBL; D84550; BAA12697.1;
 CC EMBL; D84551; BAA12698.1;
 CC EMBL; D85557; BAA12830.1;
 CC EMBL; D85558; BAA12831.1;
 CC EMBL; D85559; BAA12832.1;
 CC EMBL; U60151; AAB06616.1;
 CC EMBL; D84125; BAA12230.1;
 CC EMBL; D84126; BAA12231.1;
 CC EMBL; AB011006; BAA24899.1;
 CC EMBL; U67207; ABA04654.1;
 CC EMBL; AF007816; AAB63201.1;
 CC
 CC -----

DR InterPro: IPR001777;
 DR InterPro: IPR002465;
 DR Pfam: PF00041; fn3; 2;
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; 1;
 KW Obesity; Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;
 KW Alternative splicing.
 FT SIGNAL 1 ?
 FT CHAIN ? 1162
 FT DOMAIN ? 839
 FT TRANSMEM 840 860
 FT DOMAIN 861 1162
 FT DOMAIN 236 318
 FT DOMAIN 535 621
 FT DOMAIN 736 821
 FT CARBOHYD 55 55
 FT CARBOHYD 56 56
 FT CARBOHYD 73 73
 FT CARBOHYD 98 98
 FT CARBOHYD 187 187
 FT CARBOHYD 275 275
 FT CARBOHYD 345 345
 FT CARBOHYD 356 356
 FT CARBOHYD 431 431
 FT CARBOHYD 514 514
 FT CARBOHYD 622 622
 FT CARBOHYD 657 657
 FT CARBOHYD 668 668
 FT CARBOHYD 686 686
 FT CARBOHYD 695 695
 FT CARBOHYD 698 698
 FT CARBOHYD 726 726
 FT VARSPLIC 890 894
 FT VARSPLIC 895 1162
 FT VARSPLIC 890 892
 FT VARSPLIC 893 1162
 FT VARSPLIC 797 805
 FT VARSPLIC 806 1162
 FT VARIANT 269 269
 FT CONFLICT 2 2
 FT CONFLICT 12 12
 FT CONFLICT 34 34
 FT CONFLICT 751 752
 FT CONFLICT 846 846
 SQ SEQUENCE 1162 AA; 130832 MW; BA7AC2CA2D2E62AF CRC64;

Query Match 76.6%; Score 3342; DB 1; Length 1162;
 Best Local Similarity 76.0%; Pred. No. 1.3e-235;
 Matches 609; Conservative 74; Mismatches 116; Indels 2; Gaps 2;

QY 1 MICQKFCVLLHWEFYVITAFNLSPYTPWRFKLSMCPNPNSTYDFLLPAGLSKNTNS 60
 Db 1 MTCQKFCVLLHWEFYVITAFNLSPYTPWRFKLSMCPNPNSTYDFLLPAGLSKNTNS 60
 QY 61 NGHYETAVPEKNSGTHPSNLKTHCCFSEQRDNCSCADNTEGKTVSTVNSLVF 120
 Db 61 KGASEALVEAKENSTGIYVSELSKTHCCFQNEQNGCSALTGTEGKTLASVVKPLVF 120
 QY 121 QQIDANNITQCKGLKLCFYVESLFLNLFNRYNKHVLLVLPVLEDSPLVPQKGS 180
 Db 121 RQGVNWDIECNMKGDLTFLFICHMEPLLNPKNVDYKVVHLLYDLPVDDLPPLPKDS 180
 QY 181 FQWVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGVIFQSPKMSVQPTNMVKKPDP 240
 Db 181 FQTVQCNCVRE-CECHVPVPRKVNALLMYLEITSAGVSFQSPKMSVQPMVVKPDP 239
 QY 241 LGLHMEITDGNLKSWSPPPLVPFPLOQVQYKSESTTVIREADKIVSATSLVDSILP 300
 Db 240 LGLRMEVTDGNLKSWSQTKAPPLOQVQYKLENS-TIVREAAEIVSDTSLVDSVLP 298
 QY 301 GSSYEYQVGRKRLDGPGLWSDNSTPRVFTQDVFPPPKILTSVGSNVSFHCYKKNKI 360
 Db 299 GSSYEYQVRSKRLDGSVWSDNSLPQLFTQDVMYFPFKILTSGVSNASFCYKKNQ 358


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RESULT 6
ID IL6B_RAT STANDARD; PRT; 918 AA.
DC P40190;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE INTERLEUKIN-6 RECEPTOR BETA CHAIN PRECURSOR (IL-6R-BETA) (INTERLEUKIN
DE 6 SIGNAL TRANSDUCER) (MEMBRANE GLYCOPROTEIN 130) (GP130).
GN IL6ST.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=93052397; PubMed=1427893;
RA Wang Y., Nesbitt J.E., Fuentes N.L., Fuller G.M.;
RT "Molecular cloning and characterization of the rat liver IL-6 signal
RT transducing molecule, gp130.";
RL Genomics 14:666-672(1992).
CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. THE RECEPTOR SYSTEMS FOR
CC IL-6, LIF, OSM, CNTF, AND IL-11 CAN UTILIZE GPI30 FOR INITIATING
CC SIGNAL TRANSMISSION. BINDS TO IL-6/IL-6-R (ALPHA CHAIN) COMPLEX,
CC RESULTING IN THE FORMATION OF HIGH-AFFINITY IL-6 BINDING SITES,
CC AND TRANSDUCES THE SIGNAL. DOES NOT BIND IL-6. MAY HAVE A ROLE IN
CC EMBRYONIC DEVELOPMENT (BY SIMILARITY).
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: FOUND IN HEPATOCYTES, ASTROCYTES, FIBROBLASTS
CC AND ENDOTHELIAL CELLS.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC
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CC
DR EMBL; M92340; ; NOT_ANNOTATED_CDS.
DR PIR; A44257; A44257.
DR HSSP; P40189; 1BQU.
DR InterPro; IPR001777;
DR InterPro; IPR002465;
DR Pfam; PF00041; fn3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;
DR Repeat.
FT SIGNAL 1 22
FT CHAIN 23 918
FT DOMAIN 23 618
FT TRANSMEM 619 640
FT DOMAIN 641 918
FT DOMAIN 26 120
FT DOMAIN 124 221
FT DOMAIN 222 323
FT DOMAIN 324 422
FT DOMAIN 423 516
FT DOMAIN 517 612
FT DOMAIN 724 754
FT DISULFID 134 144
FT DISULFID 172 181
FT CARBOHYD 43 43
FT CARBOHYD 61 61
FT CARBOHYD 83 83
FT CARBOHYD 131 131
FT CARBOHYD 157 157

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FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 389 389 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 477 477 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 918 AA; 102450 MW; 9E18B6FECFF087F7 CRC64;

Query Match 6.2%; Score 270.5; DB 1; Length 918;
Best Local Similarity 22.6%; Pred. No. 5; le-12;
Matches 116; Conservative 98; Mismatches 215; Indels 85; Gaps 25;

QY 327 VFTTQDVI-----YPPKILTSVGSNVSFHCYKKNKIVPSKE---IVWMNLAEL 374
DB 14 IELTTEISQILVEPCGYIPEPVPVQSGNSFTATCVLKEKCLQVYSVATYIVWKNHV- 72
QY 375 KIPQSOYDVVSDHVSQVYTFNLTNETKPRGFTYDAVY-----CCNEHECHHRYAEIYVI- 428
DB 73 AVPKQGVTVINRTASSTVF-----TDVVFQNVQLTCNLSFGQIEQNVYGIT 119
QY 429 -----DWNINISC-ETDGYLTMTKTCRHSWTSTIQSLAESTLQIYHRSSLYCSDIPSIH 480
DB 120 ILSGYPPDIPITNLSCIVNEG---KNMLCQ-----LDPGRETLYETNYTLKSEWATE----- 167
QY 481 PISEPKDCVQLQSDGFYECI--FOPIFLSLSGYTMWIRINHSGLSDSPPTCVLPDWSVKPL 538
DB 168 ---KFPDCETK-HGTSSCMGTYPIFYVN-IEVWEAENALGNVSSEPIFNPDPVKVPS 222
QY 539 PPSSVKAETINI-GLLKISW-----EKVPFPENNLQFOIRYGLSGKEQVMKMYEYDAK 592
DB 223 PPHNLSTVNSELSILKLAWVNSGLDSTLRKSDIQVTRKDAST-----WIOVPLEDTV 277
QY 593 SKSVSLPVDL--CAVAVQVRCRLDGLGYWSNWSNAYTVVMDIKVPMRCPETWRIIN 650
DB 278 SPRTSFTVDLAPFTFYVFRINSIKENKGYWSNWESEASGTTYEDR-PSKAPSWYKVN 336
QY 651 GDTMKKEKNVTLMLKPLMKNSLCSVQRY--VINHTSCNGTWSNEDVGNHTKFTFLWTEQ 708
DB 337 ANHPQEYSARLINKTLPSEANGKILDEYVVLVTSKVSQTYTV---NGTELVNLNN 393
QY 709 AHTVTVLAINSGASVANFNLTFSHPMSKV-NIVOSLSAYPLNSSCVIVSWILSPDYLK 767
DB 394 RYVASLAARNVGVKSPATV-LTIPGSHFKASHPVVDLKAFP-KONLLWVEW--TPPSKPV 449
QY 768 MYFIEEMKNLNEDEI--KWLRISSSVKKYIYHG 799
DB 450 NKYLEWCVLSENSPCIDPWOQEDGTVNRTHLRG 483

RESULT 7
GCSR_MOUSE STANDARD; PRT; 837 AA.
ID GCSR_MOUSE
AC P40223;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE GRANULOCYTE COLONY STIMULATING FACTOR RECEPTOR PRECURSOR (G-CSF-R).
DE CSF3R OR CSFGR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90235283; PubMed=2158861;
RA Fukunaga R., Ishizaka-Ikeda E., Seto Y., Nagata S.;
RT "Expression cloning of a receptor for murine granulocyte colony-
RT stimulating factor";
RL Cell 61:341-350(1990).
RN [2]
RP STRUCTURE BY NMR OF 225-333.
RX MEDLINE=97331327; PubMed=9187659;

```


FT	DOMAIN	25	627		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEN	628	650		POTENTIAL.
FT	DOMAIN	651	836		CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	25	117		IG-LIKE C2-TYPE DOMAIN.
FT	DOMAIN	121	227		FIBRONECTIN TYPE-III.
FT	DOMAIN	228	332		FIBRONECTIN TYPE-III.
FT	DOMAIN	333	428		FIBRONECTIN TYPE-III.
FT	DOMAIN	429	525		FIBRONECTIN TYPE-III.
FT	DOMAIN	526	621		FIBRONECTIN TYPE-III.
FT	DISULFID	131	142		BY SIMILARITY.
FT	DISULFID	248	295		
FT	DISULFID	266	309		
FT	CARBOHYD	51	51		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	93	93		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	128	128		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	134	134		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	389	389		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	474	474		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	579	579		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	610	610		N-LINKED (GLCNAC. .) (POTENTIAL).
FT	VARSPLIC	750	783		VLQQLGSGTSPGGHLYRCDSQTPLAGLTPS -> AGP PRSAFYKDXQIMLPAPPNGLLCLFLPTISYL (IN ISOFORM GCSEF-4/D7).
FT	VARSPLIC	784	836		MISSING (IN ISOFORM GCSEF-4/D7).
FT	VARSPLIC	680	680		E -> ELPGPROGOWLGQTSMSRALPHPCVQ (IN ISOFORM GCSEF-3).
FT	VARSPLIC	622	836		EGSELHIILGVLGULLLTLCGTAWLCCSPNRKNPLWESV PPAHSSUGSWVPTIMEEADGLGTLPTITKLTVLEEDS KKPVWESHNSSETCGTLVTQVYLAQDPRAVSTQPQSOS GTSDVOLXQLLGSPGPGHLYRCDSQTPLAGLTPSPK SYENALFOASPLGLTVTPAPSOEDDCVFGPLNFPLOGIR VHGMAWGSP -> APTGRPSGOVSQTOLTAHAFGCCPOS WRPMSSCPALARAHPSRSSQCRRMKRSRCPGPSITQAORP ASPLMRWCMSRGTEQBPFPSPNPSLAPAIRSFMSGCAAP AQAGQISATVTPSLPSRWASRPASPMPRTSGSRPAPMGWGP (IN ISOFORM GCSEF-2).
FT	SEQUENCE	836 AA;	92156 MW;	3531ADDC979D4BC3 CRC64;	
Query Match		5.6%;	Score 242.5;	DB 1;	Length 836;
Best Local Similarity		22.7%;	Pred.No. 5e-10;		
Matches 112;	Conservative	75;	Mismatches	183;	Indels 123; Gaps
Qy	341 LTSVGSNVSPHCYIKKE-NKVPSEKIYVMMLAKIPQSOVDVVSD--HVSKVTFEFLN 397				
Db	35 IVHLGDPIITASCIIKNCSHLOPEQLWLRLG-AELQGGQRORLSOGTQESIITLPHLN 93				
Qy	398 ETRPKRGFTYDAVYCNEHECHHRVAELYVID-----VNINISCETGYLTKMT 446				
Db	94 HTQ-----AFLSC---CLNWGNLSQLLDQVELRAGYPPIAPHNLSCLMNLTTSSL 141				
Qy	447 CRWSTSTIQSLAES-TLQLRYHRSSLYCSDIP8IHPISEPKCYLSDSGYECI----- 499				
Db	142 QMEPGEPETHLPTFTLKFSKRG-----NCQTQGSILDICVPKDQGS 184				
Qy	500 -----EQPIFLLSGYTMWIRINHSLGSLDSPCTCVLPDSVVKPLPP-----SSVKAET 548				
Db	185 HCCIIPRKHLILYONMWIWOAEALGTSKSQCLDLPMDVVKLEPPMLRTMDSPEA-AP 243				
Qy	549 INGLLKISWEKPVP--ENNLOFOIRYGLSGKEYOMKWIEYDAKSVSLVPP----- 601				
Db	244 PQAGCLQLCWE-PWPQGLHINOCELRHKPQGEASNALVG-----PLPLEALQ 291				
Qy	602 -DLCAV-----YAVQVRCKRLDGLYKSNWSNPAYTVMDIKVPMRGP-----EFWRIRIN 650				
Db	292 YELCGLPATATYTLQIRCIRLWPLGHWDNS-PS-----LELRTTERAPTVLDTWVR--- 343				
Qy	651 GDPMKKEKNVTLLWKPLMKNDSLCSVQRYVINHTS-----CNGTWSEDVGNHTKF 701				
Db	344 -QROLDPRIVQLFWKVPVPLEEDSGRIQGVVYWRPSGAGAILPLCNTT-----ELSC 395				
Qy	702 TFLWTQEAHTVTVLAINSIGASVANFNLTJFSWMPSKYNIVOSAYSPLNSSCVIVSWILS 761				

DE GN RECEPTOR).

OS LIFR.

OC Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RQ SEQUENCE FROM N.A. (SECRETED FORM).

RX MEDLINE=92007727; PubMed=1915266;

RA Gearing D.P., Thut C.J., Vandenbos T., Gimpel S.D., Delaney P.B.,

RA King J., Price V., Cosman D., Beckmann M.P.;

RT "Leukemia inhibitory factor receptor is structurally related to the

RT IL-6 signal transducer, gp130.";

RL EMBO J. 10:2839-2848(1991).

RN [2]

RP SEQUENCE FROM N.A. (SECRETED FORM).

RP STRAIN=ICR; TISSUE=Liver;

RC MEDLINE=94039833; PubMed=7901054;

RX Tomida M., Yamamoto-Yamaguchi Y., Hozumi M.;

RA J. Biochem. 115:557-562(1994).

RT "Three different cDNAs encoding mouse D-factor/LIF receptor.";

CC -1- FUNCTION: SIGNAL-TRANSDUCING MOLECULE. MAY HAVE A COMMON PATHWAY

CC WITH GP130. THE SOLUBLE FORM INHIBITS THE BIOLOGICAL ACTIVITY OF

CC LIF BY BLOCKING ITS BINDING TO RECEPTORS ON TARGET CELLS.

CC -1- SUBUNIT: HETERODIMER COMPOSED OF LIFR AND GP130.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. THERE IS A

CC MEMBRANE-BOUND AND A SECRETED FORM.

CC -1- ALTERNATIVE PRODUCTS: THE SECRETED AND THE MEMBRANE-BOUND FORMS

CC MAY ARISE BY ALTERNATIVE SPLICING.

CC -1- TISSUE SPECIFICITY: PLACENTA, LIVER, KIDNEY, HEART, LUNG, BRAIN,

CC AND EMBRYOS. THE LIVER MAY BE THE PRIMARY SITE OF SYNTHESIS OF

CC THE SECRETED FORM.

CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; S73496; AAC60698.1; .

DR EMBL; S73495; AAC60697.1; .

DR EMBL; D26177; BAA05165.1; .

DR EMBL; D17444; BAA04258.1; .

DR MGD; MGI:96788; Lifr.

DR InterPro; IPR000950; .

DR InterPro; IPR00177; .

DR Pfam; PF00041; fn3; 4.

DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.

KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal;

KW Alternative splicing; Repeat.

FT SIGNAL

FT CHAIN 1 43

FT DOMAIN 44 1092

FT LEUKEMIA INHIBITORY FACTOR RECEPTOR.

FT DOMAIN 44 828

FT EXTRACELLULAR (POTENTIAL).

FT DOMAIN 829 953

FT POTENTIAL.

FT DOMAIN 854 1092

FT CYTOPLASMIC (POTENTIAL).

FT DISULFID 53 63

FT BY SIMILARITY.

FT CARBOHYD 164 164

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 199 199

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 238 238

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 261 261

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 385 385

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 402 402

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 421 421

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 440 440

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 453 453

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 476 476

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 567 567

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 647 647

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 658 658

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 675 675

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 724 724

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 782 782

FT N-LINKED (GLCNAC. .) (POTENTIAL).

FT VARSPLIC 718 719

FT AP -> EA (IN SECRETED ISOFORM).

FT VARSPLIC 720 1092

FT MISSING (IN SECRETED ISOFORM).

SQ SEQUENCE 1092 AA; 122573 MW; 6F02BBCBE154DE70 CRC64;

Query Match 4.8%; Score 208; DB 1; Length 1092;

Best Local Similarity 19.6%; Pred. No. 2.3e-07;

Matches 144; Conservative 125; Mismatches 271; Indels 196; Gaps 41;

QY 178 KGSFQMVHCNSVHECCCLVPVP-----TAK---LNDTLLMC--LKITSGVIFQSP- 225

DB 45 KRGVODLKCTTNNMRVMDCTWPAPLGVSPTVKDICKDRFHSCHPLETNNYKIPALSPG 104

QY 226 -----LMSVQPINMVKPDPPLGLHMEITDD---GNLKIWSW--PPLVPF 265

DB 105 DHEVTYNYLNGFQSFLENEKDVSLIPETPEI---LDLSADFTSLLLKWNDRGSAIPH 161

QY 266 P--LQYQVKSSENTTVIREADKIYSATSL-----VDSILPGSSYEVQVRGK 311

DB 162 PSNATWEIKVLQNPRT---EPVALVLLNTMLSGKDTQVQHNWNTSDLPQCATHSVSRW- 217

QY 312 RLDGPCI-----WSDWSTPRVET---TQDVYFPKILTSVGSNVSPHCIIYKKNKIYPS 363

DB 218 HIDSHPFGYKQWSDMSPLKNSWIRNTETNVFPQDKVVLGAGSNNTICC-----MSPT 270

QY 364 KEIVWMM-NLASKIPQSDVYVSDHVSQVTFENLNETPRGK---FYDVAVYCNEHEC 418

DB 271 KVLQSGQIGNTLRLHLHYGQTVAIH-----LNIPVSENSGTNIIFITDDV----- 317

QY 419 HRYIAEL-----YVIDVNIINISCTGYLTMTCTRWSTSTIOSL-----AESTL----- 462

DB 318 ---YGTVVFAGYPPDPVQKLSCTHD-LKEIICSNWPNRITGLVGRNTEVTLFESISGK 373

QY 463 QLRYHR-----SSLYCSDIPSHPISSEPKDCVLOSDGYECIFQFIFLLSGYTMWIRNH 517

DB 374 SAVFHRIEGLTNETYRLGV-QMHPQGEIHN-----FTLTG-----RN 409

QY 518 SLGSLDSPPTCVLPDSVVKPPLPPSSVKAIEITINIGLLKISWEKP-VFPENNLOFOIRYGL 576

DB 410 PLGOAQSAVVINVTERRA-PHDPTSLKVK-DINSVTVTFSWLPNGFTKINLLQCIETCK 467

QY 577 SKEVQWKMXYEYDAKSKSVSLPVPDL--CAYAVQVQVRCKRLDGLGYVSNMSPNAYTVVM 634

DB 468 ANSKKEVRNATIRGAEDSTYHVAVDKLNPYATYATYTRVRCSS-KTEWKWSRWSDEKRHLTT 526

QY 635 DIKVPMRGPEFWRIINGDTMKKEKAVTLLWPKMKNDSLCSQVRYVINHHSTSCNCTWSED 694

DB 527 E-ATPSKGPDTWREWSSD-----GKNLIVYWKPLPINEA-----NGKILSYNVS 571

QY 695 VGNHFKFTFLMTEQAH-----TVTVLAINISGASVANFNLTFSWPMSKVNIQVS 743

DB 572 LNEETQSVLEIFDPOHRAEIQLSKNDYIISVARNASGSSPPSKIASWEIPNDITVEQA 631

QY 744 LSAYPLNSCVIVSWILSPS---DYKLMYFIEWKVN--LNEDEIKWLRISSSVKK----- 794

DB 632 VGL-----GNRIFLTWRHDPNMTCDY-----VIKWCNRSRSEPCLLDWRKVPNSSTETVIE 682

QY 795 -----YYIHG 799

DB 683 SDQFQPGVRYNPLYG 698


```

CC EMBL; U64198; AAB36675.1;
DR HSP; P40189; 1BQ.
DR MIN; 601642;
DR InterPro; IPR001777;
DR InterPro; IPR002465;
DR InterPro; IPR002996;
DR Pfam; PF00041; fn3; 3.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 21
FT CHAIN 22 862
FT DOMAIN 22 624
FT TRANSMEM 625 641
FT DOMAIN 642 862
FT DOMAIN 224 306
FT DOMAIN 421 508
FT DOMAIN 519 607
FT CARBOHYD 48 48
FT CARBOHYD 129 129
FT CARBOHYD 166 166
FT CARBOHYD 195 195
FT CARBOHYD 271 271
FT CARBOHYD 347 347
FT CARBOHYD 376 376
FT CARBOHYD 480 480
SQ SEQUENCE 862 AA; 971134 MW; 67C0E0D946B8DD58 CRC64;

Query Match
Best Local Similarity 4.6%; Score 200.5; DB 1; Length 862;
Matches 115; Conservative 79; Mismatches 208; Indels 121; Gaps 27;

QY 332 DIVYFPFKILTSVGSVNSFHCI-----YKKNKIVPSKEIVWMNLAEKIPQSOYD 382
DB 32 DVTVKPSHVL-LGSVNITCSLKPGQCFHYSRKNLLYK-----FD 74

QY 383 -VVSDH-----VSKVTFNMLNTEKPKGTETDAVYCCNEHECHRYAEIYV--IDVNI 433
DB 75 RRIHFHGHSLNSOVTGLPTGLTFVCKLA-----CINSDEIQICQAEIFVGVAPEQPON 129

QY 434 ISCETDGLTKMTCSWTSTIQSL-AESTLQRLYHRSSLY---CSDIPSIHPISEPKDC- 488
DB 130 LSCIQKGEGTACVWGERDTHLTETYLQSLGPKNLTWQKQCKDI-----YCD 179

QY 489 YLQSDGFYECIFQIFLLSGYTWIRINHSGLSDSPCTCVLPDSVWKPPLPSSVKAET- 547
DB 180 YLD-----FGINLTSPESPESNFTAKVTAVNSLSSSLSTFTFLDIVRPLPDPWDIRIKQ 235

QY 548 TINIGLLKISWEKPPENNLOFQIRYGLSGKEVQWKMVEYVDAKSQSVLPVPLCAVY 607
DB 236 KASVSRCTLYWDEGLVLLN---RLRYPSNSRL-WNNVNTKAKGRHDLDLKPF-TEY 290

QY 608 AVQVRCKRLDGLGYNSNKNPNATVVMIDIKVPMRGP-----EFWRILNGDTAKK-----EK 658
DB 291 EQQISKHLHYKGSNDSSES-----LRAQTEEPETGMLDVW-----YMKRHIDYSRQ 339

QY 659 NYTLKWLKMLKNDSCSVQRYVINHTSCNG-TWSEDEVGNHTKFTFLWTEQAH-VTVVLA 716
DB 340 QISLFWKNSLVSSEARGKILHYQVTLQELTGKAMQNTGHTSWTVIPRYGNWAVAYSA 399

QY 717 INSIGASVANFLTSPWPKVNIY-----QSLSAYPLNSCCVIVSWILSPSD-Y 765
DB 400 ANSKGSSLP-----TRINIMNCEAGILLAPQVANSSEGMNDILVTWQPRKQPS 449

QY 766 KMYPIFKMKNLNDEG-----IKWLR-----ISSSVKY 795
DB 450 AVQEVVWEMRELHPGGDTQVPLNLRSPRYNSVALISENIKSY 492

```

RESULT 13

PRLR_MELGA

ID PRLR_MELGA STANDARD; PRT; 831 AA.

```

AC Q91094; Q91091; Q91092;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R) (TPRLR).
OS PRLR.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
TX TISSUE-Kidney;
RX MEDLINE=97057891; PubMed=8902221;
RA Zhou J.F., Zadworny D., Guemene D., Kuhnlein U.;
RT "Molecular cloning, tissue distribution, and expression of the
RT prolactin receptor during various reproductive states in Meleagris
RT gallopavo."
RL Biol. Reprod. 55:1081-1090(1996).
RN [2]
RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.
RC TISSUE-Ovary;
RA Pitts G.R., You S.K., Foster D.N., el Halawani M.E.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L76587; AAB01544.1;
DR EMBL; U22947; AAB75038.1;
DR EMBL; U22924; AAB75039.1;
DR HSP; P16471; 1BP3.
DR InterPro; IPR000950;
DR InterPro; IPR001777;
DR InterPro; IPR002465;
DR Pfam; PF00041; fn3; 4.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSMEM 439 459
FT DOMAIN 460 831
FT DOMAIN 25 122
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315
FT CARBOHYD 335 335
SQ SEQUENCE 831 AA; 94394 MW; 220916320F77FAC1 CRC64;

```

Query Match

Best Local Similarity

4.1%; Score 181; DB 1; Length 831;
20.4%; Pred. No. 1.5e-05;

01-OCT-2000 (Rel. 40, Last annotation update)
 PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATASE PHOSPHATASE)
 LAR.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90046860; PubMed=2554325;
 RA Streuli M., Krueger N.X., Tsai A.Y.M., Saito H.;
 RA "A family of receptor-linked protein tyrosine phosphatases in humans and Drosophila";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8698-8702(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CANTON-S;
 RX MEDLINE=96178473; PubMed=8598047;
 RA Krueger N.X., van Pabro D., Wan H.I., Gelbart W.M., Goodman C.S., Saito H.;
 RA "The transmembrane tyrosine phosphatase DLAR controls motor axon guidance in Drosophila";
 RL Cell 84:611-622(1996).
 CC -1- FUNCTION: IT IS POSSIBLE THAT DLAR IS A CELL ADHESION RECEPTOR. IT POSSESSES AN INTRINSIC PROTEIN TYROSINE PHOSPHATASE ACTIVITY (PTPASE). IT CONTROLS MOTOR AXON GUIDANCE.
 CC -1- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATASE + H(2)O -> PROTEIN TYROSINE + ORTHOPHOSPHATE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: SELECTIVELY EXPRESSED IN A SUBSET OF AXONS AND PIONEER NEURONS IN THE EMBRYO.
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 16 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 PROTEIN-TYROSINE PHOSPHATASE DOMAINS.
 CC
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 CC
 DR EMBL; M27700; AAC28668.1; -;
 DR EMBL; U36857; AAC47002.1; -;
 DR EMBL; U36849; AAC47002.1; JOINED.
 DR EMBL; U36850; AAC47002.1; JOINED.
 DR EMBL; U36851; AAC47002.1; JOINED.
 DR EMBL; U36852; AAC47002.1; JOINED.
 DR EMBL; U36853; AAC47002.1; JOINED.
 DR EMBL; U36854; AAC47002.1; JOINED.
 DR EMBL; U36855; AAC47002.1; JOINED.
 DR EMBL; U36856; AAC47002.1; JOINED.
 DR PIR; A36182; TDFELK.
 DR HSP; P28827; IRPW.
 DR Flybase; FBgn0000464; Lar.
 DR InterPro; IPR000242; -;
 DR InterPro; IPR000387; -;
 DR InterPro; IPR001777; -;
 DR InterPro; IPR003006; -;
 DR Pfam; PF00102; 1-phosphatase; 2.
 DR Pfam; PF00041; fn3; 9.
 DR Pfam; PF00047; fn3; 3.
 DR PRINTS; PR00014; FNTYPTII.
 DR PRINTS; PR00700; PRTYPTPTASE.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_2; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_PTP; 2.
 DR Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Cell adhesion; Immunoglobulin domain; Duplication.
 KW SIGNAL
 FT 1 32

FT CHAIN 33 2029 PROTEIN-TYROSINE PHOSPHATASE DLAR.
 FT DOMAIN 33 1377 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1378 1402 POTENTIAL.
 FT DOMAIN 1403 2029 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 50 118 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 154 216 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 249 308 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 320 417 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 418 512 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 513 607 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 608 706 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 707 809 FIBRONECTIN TYPE-III 5.
 FT DOMAIN 810 906 FIBRONECTIN TYPE-III 6.
 FT DOMAIN 907 1007 FIBRONECTIN TYPE-III 7.
 FT DOMAIN 1008 1102 FIBRONECTIN TYPE-III 8.
 FT DOMAIN 1103 1207 FIBRONECTIN TYPE-III 9.
 FT DOMAIN 1492 1738 PROTEIN-TYROSINE PHOSPHATASE.
 FT DOMAIN 1761 2029 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 1670 1670 BY SIMILARITY.
 FT ACT_SITE 1961 1961 BY SIMILARITY.
 FT DISULFID 57 111 POTENTIAL.
 FT DISULFID 151 209 POTENTIAL.
 FT DISULFID 256 301 POTENTIAL.
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 253 253 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 298 298 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 553 553 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 666 666 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 721 721 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 774 774 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 915 915 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 962 962 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1183 1183 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1304 1304 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 2029 AA; 229027 MW; 536A0C794D3DC800 CRC64;

Query Match

Best Local Similarity 3.8%; Score 166.5; DB 1; Length 2029;
 Matches 123; Conservative 119; Mismatches 257; Indels 159; Gaps 32;

QY 218 GGVIFQSPMLSVQPINMKVDPPL-----GLHMEITDGNLKIWSPPPLVFPLOYO- 270
 DB 90 GGI-----SILRIEPRVAGRDADPYECVAENGVDASADATLTIEGDKTPAGFPVITQG 145
 QY 271 --VKYSENSTVIREADKIVSATSL-----VDSILPGSSYE---VQVRGRKLDGPG 317
 DB 146 PGRVIEVGHVTLMTCKAIGNPTNIIWKQTKVMSNPYSKDGFLQIENSREEDQG 205
 QY 318 IW-----SDWSTPRVFTTQDVIYF-----PPKILTSV--GSNVSFHCYKKNK 359
 DB 206 KYECVAENSMGTESKATN--LYVKVRVPPTFSRPPETISEVMLGSLNLSIAVGS-- 261
 QY 360 IVPSEIIVWMNLAEKIQSQVDVVDVSKVTFNLMETKPRKFTYDAVYCCNEHECH 419
 DB 262 --PMHVKVMKGSDELTPENEMPIGRNVQLI---NIQES-----ANYTCAASTL 307
 QY 420 HRYAELYYIDVYNINISCTDGYLTMTKTC-----RNSTSTIQSLAESTQLRHYRSLVCS 474
 DB 308 GOIDSVSVMKVSOSLPTAPTDQISEVTATSVLEVSXKGPEDLQYVVIQYKPKNAQAFS 367
 QY 475 DIPSIHPISEPKDCYLQSDGFYECIFQPIFLLSGVTW-----IRINH--SLGSLDSPPTCV 529
 DB 368 EISGI-----ITMYVVRALSPYTEFEFVIYVAVNNIGRGPSPAPACT 410
 QY 530 LPDSVVKLPSPSSKAEITINIGLLKISWEKPVFPENNLO-FQIRYGLSGK--EYQWKY 586
 DB 411 TGETKNES-APRNQVR-TLSSSTWITWEPPTENGQVTKYKVVYTTNSNOPEASWSQ 468
 QY 587 EYDAKSKSVSLPVDLCVAVQVRCRLDGLGVLGWSNWSNPAYTVVMDIK-----VPMRG 642
 DB 469 MVDNSELTVSDVTPH--AIYTVRVQ-----AYTSMGAGPMSTPV-QVRAQCGQVSPQ 518

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 22, 2001, 16:03:50 ; Search time 24.21 Seconds
(without alignments)
2013.287 Million cell updates/sec

Title: US-09-116-676-10

Perfect score: 4363

Sequence: 1 MICQKFCVLLHWEFIYVIT.....WLRISVVKKYIIRKFTIL 804

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 6062398 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_0601.*
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22: /SIDSB/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4363	100.0	804	AAW34501	Obesity receptor p
2	4337	99.4	839	AAW34502	Obesity receptor p
3	4337	99.4	896	AAW24052	Human WSX receptor
4	4337	99.4	923	AAW24053	Human WSX receptor
5	4337	99.4	970	AAW34499	Obesity receptor C
6	4337	99.4	972	AAW34497	Obesity receptor A
7	4337	99.4	999	AAW34498	Obesity receptor B
8	4337	99.4	1165	AAW24051	Human WSX receptor
9	4337	99.4	1165	AAW113474	Peptide Seq ID No:
10	4337	99.4	1220	AAW34500	Obesity receptor D
11	4325	99.1	896	AAW50003	Human OB-R variant

12	4325	99.1	904	18	AAW50002	Human OB-R variant
13	4325	99.1	958	18	AAW38214	Human OB-R variant
14	4325	99.1	958	18	AAW31911	Human OB-R lepton
15	4325	99.1	958	18	AAW19535	Human OB-R lepton
16	4325	99.1	958	18	AAW22773	Human haematopoiet
17	4323	99.1	1165	18	AAW19116	Human OB receptor
18	4322	99.1	898	17	AAW8912	Haematopoietin rec
19	4322	99.1	908	17	AAW8911	Haematopoietin rec
20	4322	99.1	960	17	AAW8910	Haematopoietin rec
21	4315	98.9	908	18	AAW19536	Variant form of hu
22	4296	98.5	896	18	AAW14841	Human haematopoietin
23	4234	96.6	815	20	AAW05701	Human OB receptor
24	3900	89.4	1221	19	AAW62544	Human OB-receptor
25	3355	76.9	805	18	AAW22106	Murine leptin rece
26	3345	76.7	894	18	AAW24064	Murine WSX recepto
27	3345	76.7	894	18	AAW19114	Murine short form
28	3345	76.7	900	18	AAW22105	Murine leptin rece
29	3345	76.7	1162	18	AAW19115	Murine long form O
30	3342	76.6	1162	20	AAW13473	Peptide Seq ID No:
31	3342	76.6	892	18	AAW34260	Rat ob receptor is
32	3342	76.6	894	18	AAW37337	Ob protein recepto
33	3342	76.6	895	18	AAW34258	Rat ob receptor is
34	3342	76.6	1162	18	AAW34257	Rat wild-type ob r
35	3342	76.6	1162	18	AAW23398	Rat ob receptor (w
36	3336	76.5	894	18	AAW37338	Ob protein recepto
37	3336	76.5	1162	18	AAW23399	Rat ob receptor (f
38	3143	72.0	783	18	AAW24054	Murine WSX recepto
39	3039	69.7	842	18	AAW22102	Murine leptin rece
40	2772	63.5	1015	18	AAW34259	Rat ob receptor is
41	2665	61.1	883	19	AAW62543	Human ob-receptor
42	1151	26.4	235	19	AAW62545	Soluble leptin bin
43	570	13.1	581	18	AAW22103	Murine leptin rece
44	564	12.9	319	18	AAW22104	Murine leptin rece
45	351	8.0	1158	21	AAW92205	Fusion polypeptide

ALIGNMENTS

RESULT 1

AAW34501
ID AAW34501 standard; protein; 804 AA.

XX AAW34501;

XX 18-MAR-1998 (first entry)

XX Obesity receptor protein splice variant.

XX Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
XX high blood lipid level; obesity; diabetes; high cholesterol level;
XX weight loss; therapy; weight maintenance; splice variant.

XX Homo sapiens.

XX W09725424-Al.

XX 17-JUL-1997.

XX 02-JAN-1997; 97WO-US00128.

XX 31-DEC-1996; 96US-0774414.

XX 04-JAN-1996; 96US-0582825.

XX (AMGE-) AMGEN INC.

XX Chang M, Fletcher FA, Welcher AA;

XX WPI; 1997-384981/35.

XX N-PSDB; AAT98534.

XX Obesity protein receptor(s) and related DNA - used to treat weight disorders, e.g. obesity, diabetes and high cholesterol or blood

Lipid levels

Claim 4; Page 89; 151pp; English.

This sequence represents a natural splice variant of the obesity (OB) receptor protein. This sequence has one or more of the biological properties of naturally occurring OB receptor protein. The OB receptor proteins and OB receptor/OB protein complexes are used for the treatment of obesity, diabetes, high blood lipid levels and high cholesterol levels. The proteins may also be used to treat an individual for weight loss or weight maintenance required for purely cosmetic purposes.

Sequence 804 AA;

Query Match 100.0%; Score 4363; DB 18; Length 804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 804; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MICOKFCVLLHWEFIYVITAFNLSPYITPWRFKLSMPPNSTYDYFLPAGLSKNTS 60
DB 1 micqkfcvllhwefiyvitafnlspypitpwrfrklscmpnstydyflpagskntsn 60
QY 61 NGHYETAPEKFNSSGTHFNSLTKTTFHCCFRSEQRNCSLACADNIEGKTFVSTVNSLVF 120
DB 61 ngyetavepkfnssgthfnslnkttfhccfrseqrncslacdniegkftvstvnslvf 120
QY 121 QOIDANNIQCWLKGLDKLFICYVESLFKNLFNRYNFKVHLLYVLPVLEDSPLVPQKGS 180
DB 121 qqidanwniqcwlkgdlklficyveslfknlfnykvhllylvlevedsplvpqkgs 180
QY 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITNSGGVIFQSPMLSVQPINNVKPDPP 240
DB 181 fgmvhcnscvheccceclvpvptaklndtlmlckitnsggvifqspmlsvqipnmvkdpp 240
QY 241 LGHMEITDGNLKIWSPPPLVPFPLOQVQKYSNSTVIREADKIVSATSLLVDSILP 300
DB 241 lghmeitdgnlkiwsppplvpfploqvkysensttvi readkivsatsllvdsilp 300
QY 301 GSSYEVQVRGKRLDGGPINSWSTPRVFTQDVIYPPPKILTSVGSNSVFHCYKKNKI 360
DB 301 gssyevqvrgrldgpglswdstprvftqdvlyfppkiltsvgsnsvfchcykknki 360
QY 361 VPSKEIWMNNLAELIPQSOYDVSDHVSFKVTFENLNKPKGKTYDAVYCCNHECHH 420
DB 361 vpskelvwmnlaelipqsgydvsdhvsfkvtfenlnkpkrgkydavyccnehechh 420
QY 421 RYAEIYVIDVNIINISCTDGYLTCKMTSTIQSLAESTLQRLYHRSSLYCSDIPSTH 480
DB 421 ryaelyvidvniiniscetdgyltckmtcrwststiqslaestlqrlryhrsglycsdipsth 480
QY 481 PISEPKDCYLOSDGFYECIFQIFILLGYTMMIRINHSGLSDSPPTCVLPDSVYKPLPP 540
DB 481 pisepkdcylqsdgfyecifqifillsgytmvirmirinhslgsldspptcvlpdsvvykplpp 540
QY 541 SSVKAEITINIGLLKISWEKPFVPENNIFQIRYGLSGKEVQWKYEVYDAKSVSPLV 600
DB 541 ssvkaeitinigllkiswekpfvpennifqirylsgkevqwkmyevydaksvsplv 600
QY 601 PDLCAVAVQVRCKRLDGLGYWSNMSNPAYTVMDIKVPMRGPPEFWRINGDTMKKEKNV 660
DB 601 pdlcavavqvrckrldglgywsnmsnpaytvmdikvpmrgppefwrindtmkkekvn 660
QY 661 TLLWPLMKNDLSCSVQRYVINHHSTSCNGTWSDEVGNHKTFTLWTEQAHTVTVLAINSI 720
DB 661 tllwplmkndlscsvqryvinhhstscngtwsdevgnhktftlwteqahtvvtlainsi 720
QY 721 GASVANENLTFSWPNKYNIVQSISAYPLNSCVIVSWILSPSDYKLMFYIEWKNLNED 780
DB 721 gasvanenltfswpnkynivqsisayplnscvsvilspdyklymfyiewknlined 780
QY 781 GEIKWLRISSSVKKYIHGKFTIL 804
DB 781 geikwlriSSSVKKYIHGKFTIL 804

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Db 781 geikwlriSSSVKKYIHGKFTIL 804

RESULT 2

AAW34502
ID AAW34502 standard; protein; 839 AA.

XX AAW34502;

XX 18-MAR-1998 (first entry)

XX Obesity receptor protein.

XX Obesity receptor; human; OB receptor; OB receptor/OB protein complex;

XX high blood lipid level; obesity; diabetes; high cholesterol level;

XX weight loss; therapy; weight maintenance.

XX Homo sapiens.

XX W09725424-A1.

XX 17-JUL-1997.

XX 02-JAN-1997; 97WO-US00128.

XX 31-DEC-1996; 96US-0774414.

XX 04-JAN-1996; 96US-0582825.

XX (AMGE-) AMGEN INC.

XX Chang M, Fletcher FA, Welcher AA;

XX WPI; 1997-384981/35.

XX N-PSDB; AAT98532.

XX Obesity protein receptor(s) and related DNA - used to treat weight

XX disorders, e.g. obesity, diabetes and high cholesterol or blood

XX lipid levels

XX Disclosure; Page 82; 151pp; English.

This sequence represents the obesity (OB) receptor protein. This sequence was used to identify the variants shown in AAW34497-W34501. The variants have one or more of the biological properties of naturally occurring OB receptor protein. The OB receptor proteins and OB receptor/OB protein complexes are used for the treatment of obesity, diabetes, high blood lipid levels and high cholesterol levels. The proteins may also be used to treat an individual for weight loss or weight maintenance required for purely cosmetic purposes.

Sequence 839 AA;

Query Match 99.4%; Score 4337; DB 18; Length 839;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICOKFCVLLHWEFIYVITAFNLSPYITPWRFKLSMPPNSTYDYFLPAGLSKNTS 60

DB 1 micqkfcvllhwefiyvitafnlspypitpwrfrklscmpnstydyflpagskntsn 60

QY 61 NGHYETAPEKFNSSGTHFNSLTKTTFHCCFRSEQRNCSLACADNIEGKTFVSTVNSLVF 120

DB 61 ngyetavepkfnssgthfnslnkttfhccfrseqrncslacdniegkftvstvnslvf 120

QY 121 QOIDANNIQCWLKGLDKLFICYVESLFKNLFNRYNFKVHLLYVLPVLEDSPLVPQKGS 180

DB 121 qqidanwniqcwlkgdlklficyveslfknlfnykvhllylvlevedsplvpqkgs 180

QY 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLMLCKITNSGGVIFQSPMLSVQPINNVKPDPP 240

DB 181 fgmvhcnscvheccceclvpvptaklndtlmlckitnsggvifqspmlsvqipnmvkdpp 240

QY 241 LGLHMEITDDGNLKSWSPPPLVPFPLOQYQVYKSENSTTVIRADKIVSATSLVDSILP 300
 Db 241 lglhmeitddgnlkswsppplvpfploqyqvyksensttviradkivsatsllvdsilp 300
 QY 301 GSSYEVOVQRKRLDGPGLTSDWSTPRVFTTQDVVFPFKILTSVGSNVPKIKKENKI 360
 Db 301 gssyevoqvrkrlldgpgltsdwstprvfttdvvyfppfkiltsvgsnvpkikkenki 360
 QY 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSQVTFNPNLNETKPRGKFTYDAVYCCNEHECHH 420
 Db 361 vpskeiivwmnlakeipqsgdydvvsdhsqvtfnlnetkprgkftdyavycchechh 420
 QY 421 RYAEIYVIDVWININISCTDGYLTWTCRWSTSTQSLAESTLQRLYHRSSLYCSDIPSIH 480
 Db 421 ryaeliyvidvwininiscetdgyltktrwststqslaeestlqrlhrsslycsdipsih 480
 QY 481 PTSEPKDCYLQSDGFYECIFQPIFLLSGYTWIRINHSLSGLDPPPTCVLPDSVVKPLPP 540
 Db 481 ptsepkdcylqsdgyfeci fqpifllsgytwirinhslsgldppptcvlpdsvvkplpp 540
 QY 541 SSVRAEITINTGLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKVSLPV 600
 Db 541 ssvraeitintglkiskekvpfpennlqfiryglsgkevqwkmyevydaksksvslpv 600
 QY 601 POLCAVAVQVRCRLDGLGYWSNWPATVVMNDIKVPHRGPFWRILINGDTWKKKNV 660
 Db 601 polcavavqvrclrdglgywsnwpaytvmndikvphrgpfwrlingdwtmkknv 660
 QY 661 TLLWKLKNDLSLQVRYVNIHNTSCNGTSEDVGNHRTFTFLWTQAHVTVLAINSI 720
 Db 661 tllwklkndslslqvryvnihtscngtswedvgnhrtftflwtqahtvtvlainsi 720
 QY 721 GASVANFNLFSPWMSKVNIVQSLASAYPLNSSCVIVSWILSPSDYKLMFYFIEWKNLNED 780
 Db 721 gasvanfnlftspwmskvnivqslasayplnsscvivswilspdyklymfiewknlnd 780
 QY 781 GEIKWLIRISSVKKYIHGKF 801
 Db 781 geikwlirissvkkyyihdhf 801
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 ID AAW24052 standard; Protein: 896 AA.
 AC AAW24052;
 DT 17-MAR-1998 (first entry)
 DE Human WSX receptor variant 6.4.
 KW Human; WSX receptor; variant 6.4; identification; purification;
 KW ligand; activator; antibody; agonist; proliferation; obesity;
 KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
 KW type II diabetes; polycystic ovarian disease;
 KW cardiovascular disease; osteoarthritis; dermatological disorder;
 KW hypertension; insulin resistance; hypercholesterolaemia;
 KW hypertriglyceridaemia; cancer; cholelithiasis.
 OS Homo sapiens.
 PN W09725425-A1.
 PD 17-JUL-1997.
 PF 07-JAN-1997; 97WO-US00325.
 PR 20-JUN-1996; 96US-0667197.
 PR 08-JAN-1996; 96US-0585005.
 XX (GETH) GENENTECH INC.
 PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;

PI Rodrigues ML;
 XX WPI; 1997-372864/34.
 DR N-PSDB; AAT85576.
 XX WSX receptor and related antibodies and ligands - used to develop
 PT products for diagnosis and therapy, e.g. for improving
 PT haematopoiesis or for treating tumours
 XX Claim 2; Pages 86-89; 219pp; English.
 XX The present sequence is the human WSX receptor variant 6.4,
 CC which can be used to identify and purify ligands and activators.
 CC An anti-WSX receptor antibody can be used as an agonist to activate
 CC the WSX receptor, leading to enhanced proliferation or
 CC differentiation of a cell expressing the WSX receptor. It can also
 CC be used to decrease body weight and/or fat-depot weight and/or food
 CC intake in an obese mammal. WSX receptor ligands can be used to
 CC enhance proliferation or differentiation of lymphoid, myeloid or
 CC erythroid blood cell lineages. This is useful when a mammal,
 CC especially a human, is suffering from decreased blood cell levels,
 CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
 CC marrow transplantation therapy. It can also be used to repopulate
 CC blood cells in a mammal. The products can also be used to treat,
 CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
 CC polycystic ovarian disease, cardiovascular diseases,
 CC osteoarthritis, dermatological disorders, hypertension, insulin
 CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
 CC and cholelithiasis.
 XX Sequence 896 AA;
 SQ

Query Match 99.4%; Score 4337; DB 18; Length 896;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIVYITAFNLSYDITPWRFKLSCHMPNPNSTYDYELLGAGLSKNTS 60
 Db 1 micqkfcvllhwefiyvitafnlsyditpwrfklschmpnpnstydyellgagskntsns 60
 QY 61 NGHYETAPEPKFNSGTHFNSLKTTFHCGRSDRNCISLCADNIEGKTFVSNVSLVF 120
 Db 61 nghyetapepkfnsgthfnslkttfhcgrseqdrncislcadniegkftvsnslvf 120
 QY 121 QQIDANWNIQCLWLGDLKLFCTCYVESLFKFLFRNYKVLHLYLPEVLEDSPLVPQKGS 180
 Db 121 qqidanwniqclwlgdlklfcyveslfnlfrnykvhllylpevledsplvpqkgs 180
 QY 181 FQMVHCNCSVHECCCECLVPVPTAKLNDTLMLCKLITSGGVIFOSPLMSVQPINVKPDP 240
 Db 181 fqmvhcncsvheccceclvpvptaklndtlmlcklitsggvifosplmsvqipnvkpdpp 240
 QY 241 LGLHMEITDDGNLKSWSPPPLVPFPLOQYQVYKSENSTTVIRADKIVSATSLVDSILP 300
 Db 241 lglhmeitddgnlkswsppplvpfploqyqvyksensttviradkivsatsllvdsilp 300
 QY 301 GSSYEVOVQRKRLDGPGLTSDWSTPRVFTTQDVVFPFKILTSVGSNVPKIKKENKI 360
 Db 301 gssyevoqvrkrlldgpgltsdwstprvfttdvvyfppfkiltsvgsnvpkikkenki 360
 QY 361 VPSKEIVWMNLAEKIPQSQYDVVSDHVSQVTFNPNLNETKPRGKFTYDAVYCCNEHECHH 420
 Db 361 vpskeiivwmnlakeipqsgdydvvsdhsqvtfnlnetkprgkftdyavycchechh 420
 QY 421 RYAEIYVIDVWININISCTDGYLTWTCRWSTSTQSLAESTLQRLYHRSSLYCSDIPSIH 480
 Db 421 ryaeliyvidvwininiscetdgyltktrwststqslaeestlqrlhrsslycsdipsih 480
 QY 481 PTSEPKDCYLQSDGFYECIFQPIFLLSGYTWIRINHSLSGLDPPPTCVLPDSVVKPLPP 540
 Db 481 ptsepkdcylqsdgyfeci fqpifllsgytwirinhslsgldppptcvlpdsvvkplpp 540

QY 541 SSVKAEITINIGLKLISWEKVPFPENNLOFOIRYGLSGKEVQWKMVEYDAKSKVSLPV 600
 DB 541 ssvkaeitinigllkliswekvpfpennlofqirylsgkevqwmkyevydaaksksvlpv 600
 QY 601 PDLCAVAVQVRCKRLDGLGYWSNWPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
 DB 601 pdlcavavqvrckrldgldgywsnwpaytvvmdikvpmrgpewrilingdtmkkeknv 660
 QY 661 TLLWKLPMKNDLSLCSVQRYVINHHTSCNGTWSESDVGNHRTFTLWTEQAVTVVLAINSI 720
 DB 661 tllwklpmkndslcsvqryvinhhtscngtwseavgntkftflwteqavtvvlainsi 720
 QY 721 GASVANFNLTSPMPKVNIVQSLAYPLNSSCVIVSWILSPDYDKLWYFIIEWKNLNEED 780
 DB 721 gasvanfnltspmpkvnivqslaysplnsscvivswilspdydklmyfiiewknlne 780
 QY 781 GEIKWLRISSSVKYYIHGKF 801
 DB 781 geikwlrisssvkkyyihdhf 801

RESULT 4
 AAW24053
 ID AAW24053 standard; Protein; 923 AA.
 XX
 AC AAW24053;
 XX
 DT 17-MAR-1998 (first entry)
 XX
 DE Human WSX receptor variant 12.1.
 XX
 KW Human; WSX receptor; variant 12.1; identification; purification;
 KW ligand; activator; antibody; agonist; proliferation; obesity;
 KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
 KW Type II diabetes; polycystic ovarian disease;
 KW cardiovascular disease; osteoarthritis; dermatological disorder;
 KW hypertension; insulin resistance; hypercholesterolaemia;
 KW hypertriglyceridaemia; cancer; cholelithiasis.
 XX
 OS Homo sapiens.
 XX
 PN WO9725425-A1.
 XX
 PD 17-JUL-1997.
 XX
 PF 07-JAN-1997; 97MO-US00325.
 XX
 PR 20-JUN-1996; 96US-0667197.
 PR 08-JAN-1996; 96US-0585005.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Bennett B, Carter PJ, Chlang NY, Kim KJ, Matthews W;
 PI Rodrigues ML;
 XX
 DR WPI; 1997-372864/34.
 DR N-PSDB; AAT85577.
 XX
 PT WSX receptor and related antibodies and ligands - used to develop
 PT products for diagnosis and therapy, e.g. for improving
 PT haematopoiesis or for treating tumours
 XX
 PS Claim 2; Pages 89-93; 219pp; English.
 XX
 CC The present sequence is the human WSX receptor variant 12.1,
 CC which can be used to identify and purify ligands and activators.
 CC An anti-WSX receptor antibody can be used as an agonist to activate
 CC the WSX receptor, leading to enhanced proliferation or
 CC differentiation of a cell expressing the WSX receptor. It can also
 CC be used to decrease body weight and/or fat-depot weight and/or food
 CC intake in an obese mammal. WSX receptor ligands can be used to
 CC enhance proliferation or differentiation of lymphoid, myeloid or
 CC erythroid blood cell lineages. This is useful when a mammal,

CC especially a human, is suffering from decreased blood cell levels,
 CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
 CC marrow transplantation therapy. It can also be used to repopulate
 CC blood cells in a mammal. The products can also be used to treat,
 CC e.g. neoplastic disorders, arteriosclerosis, type II diabetes,
 CC polycystic ovarian disease, cardiovascular diseases,
 CC osteoarthritis, dermatological disorders, hypertension, insulin
 CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
 CC and cholelithiasis.
 XX
 SQ Sequence 923 AA;

Query Match 99.4%; Score 4337; DB 18; Length 923;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICOKFCVLLHWEFIYVITAFNLSYPITPWRFKLSMPNSTDYDFLLPAGLSKNTSNS 60
 DB 1 micokfcvllhwevlyvitatnlsyptitpwrfklsmpnstdydfllpaglskntns 60
 QY 61 NGHYTEAVPEKFNSSGTHFSNLSKTTFHCCFRSEQDRNCSLACADNIEGKTEVSTVNSLVP 120
 DB 61 nghyetavepkfnssgthfnslnskttfhccfrseqdrncslcadniegkfstvnslvf 120
 QY 121 QOIDANWNTQCLWLGDLKLFICYVESLFKNLFRNRYKVHLLYVLPVLEDSPLVPQKGS 180
 DB 121 qoidanwnlqclwlgdlklficyveslfknlfrnrykvhllylvlevedsplvpqkgs 180
 QY 181 FOMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGVIFQSPMLSVQPINMWKPDPP 240
 DB 181 fomvhcnsvheccclvpvptaklndtlmlclkitsgvifqspmlsvqipnmwkpdpp 240
 QY 241 LGLHMEITDDGNLKITSWSPPLVPPLQYQVKYSENSTTVIREADKIVSATSLVDSILP 300
 DB 241 lglhmeitddgnlkwiswspplvpplqyqvkysensttvireadkivsatsilvdsilp 300
 QY 301 GSSYEYQVGRKRLDGPGLWSWSTPRVFTQDVIYFPPKILTSVGSNSVFHCYIKKENKI 360
 DB 301 gssyeyqvrgrldgpglwsdstprvftqdviyfppkiltsgvsgnsvfhcyykknki 360
 QY 361 VPSKETVMMNLAEKIPQSDYDVSDHVSKVYTFNNLNETKPRGKTYDAVYCCNEHECHH 420
 DB 361 vpskeivmmnlaeqipsgdydvshvskvtfnnlnetkprgktydavyccnehechh 420
 QY 421 RYAELYVIDVININISCETDGYLTMTCRWSTSTIOSLAESTLQLRVHBSLYCSDIPSILH 480
 DB 421 ryaelyvidvininiscedtgyltmctcrwststioslaestlqlrhyrshslycsdipsih 480
 QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTWMIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
 DB 481 pisepkdcylqsdgfyecifqipifllsgytwmirinhslgslsdpsptcvlpdsvvkplpp 540
 QY 541 SSVKAEITINIGLKLISWEKVPFPENNLOFOIRYGLSGKEVQWKMVEYDAKSKVSLPV 600
 DB 541 ssvkaeitinigllkliswekvpfpennlofqirylsgkevqwmkyevydaaksksvlpv 600
 QY 601 PDLCAVAVQVRCKRLDGLGYWSNWPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
 DB 601 pdlcavavqvrckrldgldgywsnwpaytvvmdikvpmrgpewrilingdtmkkeknv 660
 QY 661 TLLWKLPMKNDLSLCSVQRYVINHHTSCNGTWSESDVGNHRTFTLWTEQAVTVVLAINSI 720
 DB 661 tllwklpmkndslcsvqryvinhhtscngtwseavgntkftflwteqavtvvlainsi 720
 QY 721 GASVANFNLTSPMPKVNIVQSLAYPLNSSCVIVSWILSPDYDKLWYFIIEWKNLNEED 780
 DB 721 gasvanfnltspmpkvnivqslaysplnsscvivswilspdydklmyfiiewknlne 780
 QY 781 GEIKWLRISSSVKYYIHGKF 801
 DB 781 geikwlrisssvkkyyihdhf 801

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RESULT 5
AAW34499
ID AAW34499 standard; protein; 970 AA.
XX
AC AAW34499;
XX
DT 18-MAR-1998 (first entry)
XX
DE Obesity receptor C protein.
XX
KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
KW high blood lipid level; obesity; diabetes; high cholesterol level;
KW weight loss; therapy; weight maintenance.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 959 /label= "unknown"
FT /note= "encoded by stop codon"
XX
PN W09725424-A1.
XX
PD 17-JUL-1997.
XX
PF 02-JAN-1997; 97WO-US00128.
XX
PR 31-DEC-1996; 96US-0774414.
XX
PR 04-JAN-1996; 96US-0582825.
XX
PA (AMGE-) AMGEN INC.
XX
PI Chang M, Fletcher FA, Welcher AA;
XX
DR WPI; 1997-384981/35.
XX
DR N-PSDB; AAT98530.
XX
PT Obesity protein receptor(s) and related DNA - used to treat weight
PT disorders, e.g. obesity, diabetes and high cholesterol or blood
PT lipid levels
XX
PS Claim 2; Page 72; 151pp; English.
XX
CC This sequence represents the obesity (OB) receptor C protein. This
CC sequence has one or more of the biological properties of naturally
CC occurring OB receptor protein. The OB receptor proteins and OB
CC receptor/OB protein complexes are used for the treatment of obesity,
CC diabetes, high blood lipid levels and high cholesterol levels. The
CC proteins may also be used to treat an individual for weight loss or
CC weight maintenance required for purely cosmetic purposes.
XX
SQ Sequence 970 AA;

Query Match 99.4%; Score 4337; DB 18; Length 970;
-Best Local Similarity 99.8%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFLYVITAFNLSPITPWRKLSKMPNPNSTYDFLLPAGLSKNTS 60
DB 1 micqkfcvllhweflyvitafnlspitpwrklskmpnpnstydfllpaglsknts 60
QY 61 NGHYETAPEKFNSSGTHFNSLKTTFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
DB 61 nghyetavepkfnssgthfnslnkttfhccfrseqdrncslcadniegktfvstvnslvf 120
QY 121 QQIDANNIQCWLKGLDLFCYVESLFLKRLFRNYKVHLLYVLPVLESDSLVPQKGS 180
DB 121 qqidanwniqcwlkglldlfcyveslflkrlfrnykvhllylvlevedslvpqkgs 180
QY 181 FQWVHCNCSVHECECLVPVPTAKLNDTLMLKITSGGVIFQSPMLSVQPINWPKDPP 240
DB 181 fqwvhcnscsvhececlvpvptaklndtlmlclkitsggvifqspmlsvqipnwvkdpp 240

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DB 181 fqmvhcnscsvhececlvpvptaklndtlmlclkitsggvifqspmlsvqipnwvkdpp 240
QY 241 LGLHMEITDDGNLKISWSSPPLVPFPLQYQVKYSENSTTVIREADKIVSATSLSLVDSLTP 300
XX
DB 241 lglhmeitddgnlkiswsspplvpfpfqyqvkysensttvireadkivsatllvdsilp 300
XX
QY 301 GSSYEVOVRGKRLDGPGLWSDWSTPRVFTTQDVIFPPKILTSVGSNVSFHCYKKNKI 360
DB 301 gssyevovrgrldgpglwsdwtprvfttqdvifppkiltsvgsnvsfchcykknki 360
XX
QY 361 VPSKEIYVMNNAEKIPQSOYDVVSDHVSQVTFPFLNETPRGKFTYDAVYCCNEHECHH 420
DB 361 vpskeiyvmnnlaekipqsoydvvdhsvskvtfpflnetprgkftdyavycnehechh 420
XX
QY 421 RYAEIYVIDVNIINISCTDGYLTMTCTCRWSTSTIQSLAESTLQRLYRHSLSYSDIPSII 480
DB 421 ryaeliyvidvniiniscetdgyltmtcrwststiqslaestlqlryhrsslycsdipsih 480
XX
QY 481 PISEPKDCYLQSDGFYECIFQIFLLSGYTMWIRINHSLSLSDSPPTCVLPDSVVKPLPP 540
DB 481 pisepkdcylqsdgfyecifqifllsgytmwirinhsldspptcvipldsvvkplpp 540
XX
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
DB 541 ssvkaeitinigllkiswekvpfpennlqfairyglsgkevqwmvevydaksksvslpv 600
XX
QY 601 PDLCAVYAVQVRCKRLDGLGYWSNMPAYTVVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
DB 601 pdlcavyavqvrckrldglgywsnmpaytvvmdikvpmrgpewfwiingdtmkkekvn 660
XX
QY 661 TLLWKPLMKNDLSICSVORYVINHHTSCNGTWSVDGNGHRTFTFLWTEQAHVTVVLAINSI 720
DB 661 tllwkpmlkndlsicsvoryvinhhtscngtwsedvgnhtkftflwteqahvtvvlainsi 720
XX
QY 721 GASVANPLTFSWPMKSNVQSLSAVPLNSCVIVSWILSPSDYKLMYFTIEWKNLINED 780
DB 721 gasvanpltfswpmksknvqslsavlplnscviviwslpsdyklmyftiewknlined 780
XX
QY 781 GEIKWLRISSSVKKYIYHGF 801
DB 781 geikwlri:sssvkkyihghf 801

RESULT 6
AAW34497
ID AAW34497 standard; protein; 972 AA.
XX
AC AAW34497;
XX
DT 18-MAR-1998 (first entry)
XX
DE Obesity receptor A protein.
XX
KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
KW high blood lipid level; obesity; diabetes; high cholesterol level;
KW weight loss; therapy; weight maintenance.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 897 /label= "unknown"
FT /note= "encoded by stop codon"
FT Misc-difference 919 /label= "unknown"
FT /note= "encoded by stop codon"
FT Misc-difference 925 /label= "unknown"
FT /note= "encoded by stop codon"
FT Misc-difference 939 /label= "unknown"
FT /note= "encoded by stop codon"
FT Misc-difference 948 /label= "unknown"

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FT /label= unknown
 FT /note= "encoded by stop codon"
 FT Misc-difference 952
 FT /label= unknown
 FT /note= "encoded by stop codon"
 FT Misc-difference 971
 FT /label= unknown
 FT /note= "encoded by stop codon"
 XX

W09725424-AL.

PN

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PD

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Obesity protein receptor(s) and related DNA - used to treat weight disorders, e.g. obesity, diabetes and high cholesterol or blood lipid levels

Claim 1; Page 64; 151pp; English.

This sequence represents the obesity (OB) receptor A protein. This sequence has one or more of the biological properties of naturally occurring OB receptor proteins. The OB receptor proteins and OB receptor/OB protein complexes are used for the treatment of obesity, diabetes, high blood lipid levels and high cholesterol levels. The proteins may also be used to treat an individual for weight loss or weight maintenance required for purely cosmetic purposes.

Sequence 972 AA;

Query Match 99.4%; Score 4337; DB 18; Length 972;
 Best Local Similarity 99.8%; Pred. NO. 0;
 Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSYPTIPWRFKLSMPNSTYDFLLPAGLSKNTS 60
 Db 1 micqkfcvllhwefiyvitafnlsyptipwrfklsmpnstydfllpaglsknts 60

QY 61 NGHYETAVEPKNSGTHFSNLSKTTFFHCCFRSEQRNCSLCADNTEGKTFVSTVNSLVF 120
 Db 61 nghyetavepkfnsqthfsnlskttffhccfrseqrncslcadniegkftvstvnslvf 120

QY 121 QOIDANNIQCWLKGLKLFICYVESLFLKRNRYKVVHLLVLPVLEDSPLVPQKS 180
 Db 121 qoidanniqcwlkglklficyveslflkrrnykvhllylvpvleedsplvpqks 180

QY 181 FQVHNCNSVHECCCLVFPVPTAKLNDTLLMCLKITSGGVIFQSPLSMVSQPINVVKPDPP 240
 Db 181 fqmvhncnsvehccclvfpvptaklndtllmclkitsggvifqspplmsvqpinmvkpdpp 240

QY 241 LGLHMEITDGNLKIWSGPPVLPVFPLOVQVYSENSTTVIREADKIVSATSLLVDSILP 300
 Db 241 lglhmeitdgnlkiwsppvpfploqvkyseussttviereadkivsatsllvdsilp 300

QY 301 GSSYEVQVGRKLDGPGIHSNDSTRVFTTQDVIYFPKILTSVGSNSVHFCHYKKNKI 360
 Db 301 gssyevqvgkrlldgpgilswdstvrvfttqdvlyfppkiltsvgsnsvhfchlykknki 360

QY 361 VPSKEIVWMNLAEKIPQSOYDWSHDVSKVTFENLNKPKRGKTYDQVYCCNEHECHH 420
 Db 361 vpskelvwmnlakelpsqdydwsdvskvtfenlnkprgktydavyccnehechh 420

QY 421 RYAEVYVIDVNIINISCTDGYLTMTCTRWSTSTQISLAESTLQLRVHRSSLYCSDIPSIH 480
 Db 421 ryaelvyvidvniiniscetdgyltmctcrwststqislaestlqlyrhrsslycsdipslh 480

QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGTTWIRINHSLSGLSDSPPTCVLPDSVWKPPLP 540
 Db 481 pisepkdcylqsdgfyecifqpifllsgytmwirinhsqslsdspptcvlpdsvwkpplp 540

QY 541 SSVKAETITNIGLLKISWEKPPENNLQFIQIRYGLSGREVQHKMYEVYDAKSKSVSLPV 600
 Db 541 ssvkaeitnigllkisswekppennlqfiryglsgevqhkmyevydaaksksvslpv 600

QY 601 PDLCAVYAVQVRCRLDGLGYNSNPNAYTVVMDIKVPMRGPEFWRIINGDPMKKEKNV 660
 Db 601 pdlcavyavqvrckrlldggywnsnpnaytvvmdikvpmrgpefwringdpmkkeknv 660

QY 661 TLLWKPLMKNDSLCVQRYVINHTSCNGTWSGVNHTKFTFLMTEQAHTVTVLAINSI 720
 Db 661 tllwkplmkndslcsqrvyvinhtscngtwsedvgnhckftflwteqahtvtvlainsi 720

QY 721 GASVANFNLTFSPMSKVNIVQSLSAYPLNSCVIYVSWILSPSDYKLMYFIIEWKNLNE 780
 Db 721 gasvanfnltfswmskvnivqslsayplnscvivyvswilspdyklymfiiewknlne 780

QY 781 GEIKWLIRISSVKKYVYHGKF 801
 Db 781 geikwlirissvkkyyihdhf 801

RESULT 7

AAW34498

ID AAW34498 standard; protein; 999 AA.

XX AAW34498;

XX

DT 18-MAR-1998 (first entry)

DE Obesity receptor B protein.

KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;

KW high blood lipid level; obesity; diabetes; high cholesterol level;

KW weight loss; therapy; weight maintenance.

XX Homo sapiens.

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DR WPI: 1997-384981/35.
DR N-PSDB; AAT98529.

PT Obesity protein receptor(s) and related DNA - used to treat weight
PT disorders, e.g. obesity, diabetes and high cholesterol or blood
PT lipid levels

PS Claim 2; Page 68; 151pp; English.

XX This sequence represents the obesity (OB) receptor B protein. This
CC sequence has one or more of the biological properties of naturally
CC occurring OB receptor protein. The OB receptor proteins and OB
CC receptor/OB protein complexes are used for the treatment of obesity,
CC diabetes, high blood lipid levels and high cholesterol levels. The
CC proteins may also be used to treat an individual for weight loss or
CC weight maintenance required for purely cosmetic purposes.

XX Sequence 999 AA;

Query Match 99.4%; Score 4337; DB 18; Length 999;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSPYTPWRKFLSCMPNSTDYFLLPAGLSKNTSNS 60

DB 1 micqkfcvllhwefiyvitafnlspypwrfklscompnstydyfllpaglskntcns 60

QY 61 NGHYETAVERPKFNSSGPHFNLSKTTFFHCCFRSEQDNRNCSLCADNIEGRTFVSTVNSLVF 120

DB 61 nghyetavpknssgphfnlskttffhccfrseqdncslcadniegkrtfvstvnslvf 120

QY 121 QQIDANNIOCLWKGDLKFLICVVSLEFKLFRNYKVVHLLYVLPVLEDSLPVPOKGS 180

DB 121 qqidanncioclwkgdlkflcivvslefklnynkvhllylvpvlvledslvpokgs 180

QY 181 FQMVHNCVSHECECIVPVPTAKLNDTLMLCKITSGGVIFQSPMSVQPINNVKPDPP 240

DB 181 fqmvhncvshececihpvtaklndtlmlckitsggvifqspmsvqipnmvkdpp 240

QY 241 LGLHMEITDGNLKISWSSPPLVPFLOQVQVYSENSTTVIREADKIVSATSLVDSILP 300

DB 241 lglhmeitdgnlkiswssplvpfllqyqvksensttvireadkivsatsllvdsilp 300

QY 301 GSSYEVQVRGKRLDGPGLNSDQSTPRVETQDVLYEPPKTLTSGVSNVSPHCYKKNKI 360

DB 301 gssyevqvrgrldgpglinsdqstprvettodvlyeppkltltsvsgnsvphciykkenki 360

QY 361 VPSKEIYVWNNLAEKIPQSOYQVYVSDHVSQVTFPFLNETKPRGKFTYDAVYCCNEHECHH 420

DB 361 vpskelvwmnlaekipqsgdyvvsdhvskvtfpflnetkprgkfydavyccnehechh 420

QY 421 RYAEIYVIDVNNISCEGTGTLTKWCRNSTSTIQSLAESTLQLYHRSLYCSIDPSIH 480

DB 421 ryaeliyvidvnniscedgtlktmcrnststiqslaestlqlryhrsllycsdpsih 480

QY 481 PISEPKDCYLOSGDFECLFQPIFTLLSGYTWIRINHSIGLSLDSPTCVLPDSVVRPLPP 540

DB 481 pisepkdcylsgdfecfqlpiftllsgytwirinhslgslsdspctcvlpdsvvrplpp 540

QY 541 SSVKAEITINIGLLKISWEKPPVPPENNLQFQIRYGLSGKEVQWKEVYDAKSKVSLPV 600

DB 541 ssvkaeitinigllkswepvpvppennlqfqiiryglsgkevqwkvevydaksksvslpv 600

QY 601 PDLCAVAVQVRCKRLDGLGYWSNNSPAYTVVMDIKVPMRGPEFWRIRINDGTMKKEKV 660

DB 601 pdlcavavqvrckrldglgywsnnsPAYTVVMDIKVPMRGPEFWRIRINDGTMKKEKV 660

QY 661 TLLWPKLMDKSLCSQVRYVINHTSCNGTWSQDVGNNHKTFFLTQEAHTVTVLAINSI 720

DB 661 tllwplkmdkslcsqrvyvinhtscngtwsdvgnnhktffltwqeahtvtvlainsi 720

QY 721 GASVANFNLTFSWPMKVNIVQSLAYSAYPLNSSCVIVSWILSPSDYKLMFYIIEWKNLINED 780

DB 721 gasvanfnltfswpmkvnivqslaysayplnsscvivswilspdykmyfiwknined 780

QY 781 GEIKWLRISSSVKKYYIHGKF 801

DB 781 geikwlrissssvkkyyihdhf 801

RESULT 8

AAW24051

ID AAW24051 standard; Protein; 1165 AA.

XX AAW24051;

XX 17-MAR-1998 (first entry)

XX Human WSX receptor variant 13.2.

XX Human: WSX receptor; variant 13.2; identification; purification;
KW ligand; activator; antibody; agonist; proliferation; obesity;
KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
KW Type II diabetes; polycystic ovarian disease;
KW cardiovascular disease; osteoarthritis; dermatological disorder;
KW hypertension; insulin resistance; hypercholesterolaemia;
KW hypertriglyceridaemia; cancer; cholelithiasis.

XX Homo sapiens.

OS W09725425-A1.

PN 17-JUL-1997.

XX 07-JAN-1997; 97WO-US00325.

XX 20-JUN-1996; 96US-0667197.

PR 08-JAN-1996; 96US-0585005.

XX (GETH) GENENTECH INC.

PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;

PI Rodrigues ML;

XX WPI: 1997-372864/34.

DR N-PSDB; AAT85575.

XX WSX receptor and related antibodies and ligands - used to develop
PT products for diagnosis and therapy, e.g. for improving
PT haematopoiesis or for treating tumours

XX Claim 2; Pages 81-85; 219pp; English.

XX The present sequence is the human WSX receptor variant 13.2,
CC which can be used to identify and purify ligands and activators.
CC An anti-WSX receptor antibody can be used as an agonist to activate
CC the WSX receptor, leading to enhanced proliferation or
CC differentiation of a cell expressing the WSX receptor. It can also
CC be used to decrease body weight and/or fat-depot weight and/or food
CC intake in an obese mammal. WSX receptor ligands can be used to
CC enhance proliferation or differentiation of lymphoid, myeloid or
CC erythroid blood cell lineages. This is useful when a mammal,
CC especially a human, is suffering from decreased blood cell levels,
CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
CC marrow transplantation therapy. It can also be used to repopulate
CC blood cells in a mammal. The products can also be used to treat,
CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
CC polycystic ovarian disease, cardiovascular diseases,
CC osteoarthritis, dermatological disorders, hypertension, insulin
CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
CC and cholelithiasis.

XX Sequence 1165 AA;

SQ

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Query Match      99.4%; Score 4337; DB 18; Length 1165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRKLSKMPNSTDYDFLLPAGLSKNTS 60
DB 1 micqkfcvllhwefiyvitafnlspitpwrklskmpnstdydfllpaglsknts 60
QY 61 NGHYETAPEKFNSSGTHFSNLSTKTHCCFRSEQDNCNLSLADNIEGKTFVSTVNSLVF 120
DB 61 ngyetavepkfnssgthfnslnstktthccfrseqdnrcnslcadniegktfvstvnslvf 120
QY 121 QQIDANNIQCWLKGLKLFICVYESLFKNLFNRYNYKVHLLYVLEVEDSPVLPQKGS 180
DB 121 qqidanwniqcwlkglklficyveslfknlfirnynykvhllylvlevedsplvpqkgs 180
QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGVIFQSPVLMVQPINMVKPDPP 240
DB 181 fgmvhcnscvheccclvpvptaklndtlmlckitsgvifqspvlmsvqpinmvpkdpdp 240
QY 241 LGLHMEITDGNLKIWSPPPLVPFPLOQYKYSNSTVIREADKIVSATSLLVDSILP 300
DB 241 lglhmeitdgnlkiwsppplvpfploqykyssenstvireadkivsatsllvdsilp 300
QY 301 GSSYEYQVRKRLDGPGLWSDSWSTPRVFTTQDVIFPFPKILTSVGSNVSFHCYKKNKI 360
DB 301 gssyeqvvrkrlldgpglwdsdswstprvfttqdvifpfpkiltsvgsnvsfhyckknki 360
QY 361 VFSKETVWMNLAEKIPQSOYDVSDHVSKVTFNLLNETKPRGKTYDAVYCCNHECHH 420
DB 361 vpskeivwmnlaelkipsqdydvshsvskvtfnnlnetkprgkydavyccnehechh 420
QY 421 RYAEIYVDVNIINISCTDGYTKTCRWSTSTIQSLAESTIQLRYHRSLSYCSIPSIH 480
DB 421 ryaeliyvdvniiniscetdgytktrcwststiqslaeestiqlryhrslsycsdpsih 480
QY 481 PTSEPKDCVLOSDGVECFQPIELLGVTWIRNHSIGSLDSPTCVLPDSVVKPLPP 540
DB 481 ptsepkdcvlosdgvecfqpiellgvtwirnhsigslsdptcvlpdsvvkplpp 540
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLFQIRYGLSGKEVQWKMVEYVDKSKSVSLPV 600
DB 541 ssvkaeitinigllkiswekvpfpennlfqiryglsgkevqwmvevydksksvslpv 600
QY 601 PDLCAVYAVQVRCKRLDGLGVTWNSNPAITVVMYDKIVPMRGPEFWRINGDTMKKEKNV 660
DB 601 pdlcavyavvrckrldglgvtwnsnpaitvvmymdkivpmrgpefwringdtmkkeknv 660
QY 661 TLLWKLPMKNDLSLCSVQRYVINHHTSCNTRWSDVGNHTKFTFLTEQAHTVTVLAINSI 720
DB 661 tllwklpmkndslcsvqryvinhhtscntrwsvdvgntkftflteqahtvtrlainsi 720
QY 721 GASVANFNLTFSWPMKSNVNIQSLISAYPLNSSCVIVSWILSPSDYKLMVFIEWKNLNE 780
DB 721 gasvanfnltfswpmksnvniqslisayplnsscvivswilspdyklmvfiewknlne 780
QY 781 GEIKWLRISSVKKYYIHGKF 801
DB 781 geikwlrisssvkkyyihdhf 801

RESULT 9
AA113474
ID AA113474 standard; Protein; 1165 AA.
XX
AC AA113474;
XX
XX
XX
XX 26-JUL-1999 (first entry)
XX
DE Peptide Seq ID No: 4 of WO9923493.
XX
XX Leptin; phosphorylated leptin receptor; tyrosine phosphatase ID; PTP-ID;
KW modulator; drug; weight loss; adiposity; hypertension; heart disease;
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KW type II diabetes; cancer; AIDS; agriculture.
XX Homo sapiens.
XX WO9923493-Al.
XX 14-MAY-1999.
XX 27-OCT-1998; 98WO-US22797.
XX 26-OCT-1998; 98US-0178691.
PR 31-OCT-1997; 97US-0961809.
XX (UYRQ) UNIV ROCKEFELLER.
PI Friedman JM, Li C;
XX WPI; 1999-327025/27.
DR N-PSDB; AAX55588.
XX
XX Identifying modulators agents that modulate leptin activity
XX Disclosure; Page 77-84; 96pp; English.
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The invention provides a method for identifying modulators of binding of a phosphorylated leptin receptor with tyrosine phosphatase ID PTP-ID). The method comprises: (a) contacting a tyrosine-985 phosphorylated leptin receptor or its phosphorylated fragment with protein PTP-ID or its fragment in the presence and absence of a candidate agent under conditions in which in the absence of the agent the binding of the phosphorylated leptin receptor or fragment with PTP-ID or its fragment can be detected; and (b) detecting the binding of the phosphorylated leptin receptor and PTP ID; where an increase in binding detected in the presence of the agent, indicates that the agent enhances binding, and a decrease in binding in the presence of the agent indicates that the agent is a binding inhibitor. Modulators of tyrosine-985-phosphorylated leptin receptor-dependent PTP-ID phosphorylation are useful as drugs in weight loss diet regimens. The drugs identified can regulate adiposity and fat content of animals, particularly in mammals. Disorders that can be treated by PTP-ID modulators include obesity and its associated diseases, e.g. hypertension, heart disease and type II diabetes, and weight loss associated with cancer and AIDS. Additionally the agents identified may be useful in agriculture where body weight of domestic animals can be modulated.

Sequence 1165 AA;

```
Query Match      99.4%; Score 4337; DB 20; Length 1165;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIYVITAFNLSPITPWRKLSKMPNSTDYDFLLPAGLSKNTS 60
DB 1 micqkfcvllhwefiyvitafnlspitpwrklskmpnstdydfllpaglsknts 60
QY 61 NGHYETAPEKFNSSGTHFSNLSTKTHCCFRSEQDNCNLSLADNIEGKTFVSTVNSLVF 120
DB 61 ngyetavepkfnssgthfnslnstktthccfrseqdnrcnslcadniegktfvstvnslvf 120
QY 121 QQIDANNIQCWLKGLKLFICVYESLFKNLFNRYNYKVHLLYVLEVEDSPVLPQKGS 180
DB 121 qqidanwniqcwlkglklficyveslfknlfirnynykvhllylvlevedsplvpqkgs 180
QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGVIFQSPVLMVQPINMVKPDPP 240
DB 181 fgmvhcnscvheccclvpvptaklndtlmlckitsgvifqspvlmsvqpinmvpkdpdp 240
QY 241 LGLHMEITDGNLKIWSPPPLVPFPLOQYKYSNSTVIREADKIVSATSLLVDSILP 300
DB 241 lglhmeitdgnlkiwsppplvpfploqykyssenstvireadkivsatsllvdsilp 300
QY 301 GSSYEYQVRKRLDGPGLWSDSWSTPRVFTTQDVIFPFPKILTSVGSNVSFHCYKKNKI 360
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Db 301 gssyevvrgkridgpgiawdstprvftqdvifppkiltsvgsnsvsfhcykkan1 360
QY 361 VPSKEIYWMNLAEPQSDYDVVSDHVSQVTFENLTKPRGFTYDAVYCCNEHECHH 420
Db 361 vpskeiYwmnlaepqsdYdvVsdHvsqVtFenlTKpRGfTYdAVYCCnEHechH 420
QY 421 RYAEIYVIDVINISCTDGLYKMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSII 480
Db 421 ryaeIyvidvinisctdglYkMTcrWststIQslAestlQrlYhrsslycsdipSIh 480
QY 481 PISPEKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLGSLDSPPTCVLPDSVVRPLPP 540
Db 481 piSepkdcylQsdgfYecifqPIflSGytmwIRinhslGslDSPptcVlpdsVvrPlpp 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
Db 541 ssvkaeITinigllkISwekPvFPennLOfQIRyGLsgKEvQwkmVEyDAKsksvslpV 600
QY 601 PDLCAVAVQVRKRLDGLGYWNSNPATVYVMDIKVPMRGPEFWRIINGDTMKKEKNV 660
Db 601 pdlcavavQvrKrlDglGYwnSNpATvYvMDIKvPMrgPEfWRIIngDTmkKeKnV 660
QY 661 TLAWKPLMKNDSLCSVQRVYVNHHTSCNGTWSEDVGNHTKFTTLWTEQAHVTVLAINSI 720
Db 661 tLwkpLmkndSLcsvQRvYvNHhtSCngTWsedVgnHTkFTTLwTEqAhVTVlAINsI 720
QY 721 GASVANFNLTFSWPMKVNIVQSLAYPLMSSCVIVSWILSPSDYKLMYPIIEWKNLNE 780
Db 721 gasvanfnLTfswpmKvnIVqSLayPlmSScVivswILSPsdYkLMYPIIEWknLnEd 780
QY 781 GEIKWIRISSVKKYIHGKF 801
Db 781 geikwIrissvKkyIHdhf 801

RESULT 10
AAW34500
ID AAW34500 standard; protein; 1220 AA.
XX AC AAW34500;
XX 18-MAR-1998 (first entry)
XX DE Obesity receptor D protein.
KW Obesity receptor; human; OB receptor; OB receptor/OB protein complex;
KW high blood lipid level; obesity; diabetes; high cholesterol level;
KW weight loss; therapy; weight maintenance.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 1...1165 /note= "encoded by AAT98531"
FT Misc-difference 1166 /label= "unknown"
FT Misc-difference 1169 /note= "encoded by stop codon"
FT Misc-difference 1169 /label= "unknown"
FT Misc-difference 1187 /note= "encoded by stop codon"
FT Misc-difference 1187 /label= "unknown"
FT Misc-difference 1207 /note= "encoded by stop codon"
FT Misc-difference 1207 /label= "unknown"
FT Misc-difference 1...1165 /note= "encoded by stop codon"
FT Misc-difference 1...1165 /note= "encoded by AAT98531"
XX W09725424-A1.
XX 17-JUL-1997.
PD

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XX 02-JAN-1997; 97WO-US00128.
XX 31-DEC-1996; 96US-0774414.
PR 04-JAN-1996; 96US-0582825.
XX (AMGE-) AMGEN INC.
XX Chang M, Fletcher FA, Welcher AA;
XX WPI: 1997-384981/35.
DR N-PSDB; AAT98531.
XX Obesity protein receptor(s) and related DNA - used to treat weight
PT disorders, e.g. obesity, diabetes and high cholesterol or blood
PT lipid levels
XX Claim 31; Page 76; 151pp; English.
XX This sequence represents the obesity (OB) receptor D protein. This
CC sequence has one or more of the biological properties of naturally
CC occurring OB receptor protein. The OB receptor proteins and OB
CC receptor/OB protein complexes are used for the treatment of obesity,
CC diabetes, high blood lipid levels and high cholesterol levels. The
CC proteins may also be used to treat an individual for weight loss or
CC weight maintenance required for purely cosmetic purposes.
XX Sequence 1220 AA;
SQ
Query Match 99.4%; Score 4337; DB 18; Length 1220;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MICQKFCVLLHWEFLYVITAENLSYPITPWRFKLSCMPNSTYDYFLLPAGLSKNTS 60
Db 1 micqKfcvllHweflyvItaEnlsyPiTpwRfKlScmpnStydyfllPaGlSkntS 60
QY 61 NGHYTEAVBPKFNSSGTHFSNLSKTTFFHCCFRSEQDRNCSLCADNIEGKTFVSTVNSLVF 120
Db 61 nghyETAveBpKfNssGthfSNlsKttffHccfrSEqdRncslcadnIEgKtfvstVnslVf 120
QY 121 QOIDANWNTQCLWKDGLKLFICYVESLFPKNLFRNRYKVHLLYVLPDEVLEDSPLVPQKGS 180
Db 121 qoidAnwnTqclWkDglKlFicyvEsLfpKnLfrnRykvHllyVlpDevLEdsPlvpqKgs 180
QY 181 FQMVHNCNSVHECCCECLVPVPTAKLNDTLMLCLKITSGGVIFQSPILMSVQPIVMVKKPDP 240
Db 181 fqmvHncnsVheccceclVpVptAKlNDtLmclKlItSGgvIFqSPiLMSvQPIvmVkkPdp 240
QY 241 LGLHMEITDDGNLKITSWSSPPLVPFPLOQYQVYSENSTTVIREADKIVSATSLLVDSILP 300
Db 241 lglhmeITddgnLkITswSSpPlvpfpLoqYqVysensttvIreAdKivsatsllVdsilp 300
QY 301 GSSYEVQVRGKRLDGPGLWSNDSPTPRVFTTQDVIFPPKILTSVGSNSVSHCIYKKNKI 360
Db 301 gssyevQvrGkrlDgpglWsdNstprVftTqdviFppKilTSvgSnsVshciYkKnki 360
QY 361 VPSKEIYWMNLAEKIPQSDYDVSDHVSQVTFENLTKPRGFTYDAVYCCNEHECHH 420
Db 361 vpskeiYwmnlaekIpQsdYdvSdHvsqVtFenlTKpRGfTYdAVYCCnEHechH 420
QY 421 RYAEIYVIDVINISCTDGLYKMTCRWSTSTIQSLAESTLQRLYHRSSLYCSDIPSII 480
Db 421 ryaeIyvidvinisctdglYkMTcrWststIQslAestlQrlYhrsslycsdipSIh 480
QY 481 PISPEKDCYLQSDGFYECIFQPIFLSGYTMWIRINHSLGSLDSPPTCVLPDSVVRPLPP 540
Db 481 piSepkdcylQsdgfYecifqPIflSGytmwIRinhslGslDSPptcVlpdsVvrPlpp 540
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
Db 541 ssvkaeITinigllkISwekPvFPennLOfQIRyGLsgKEvQwkmVEyDAKsksvslpV 600

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QY 601 PDLCAVAVQVRCRLDGLGYWSNWNPAFTVVMQIKVPMRGPEFWRIINGDTMKKEKNV 660
 Db 601 pdlcavavqvrckridgigyswnwnpavtvmidkvpmrspgefwrilngdtkmkeknv 660
 QY 661 TLLWKPLMKNDLSVQRYVINHTSCNGTWSVDGNGHKTFTLWTEQAHVTVLAINSI 720
 Db 661 tllwplmkndslcsqrvyvinhtscngtwsedvgnhktftlwteqahvvtvainsi 720
 QY 721 GASVANFNLTFSWPMKSNVIVQSLSAYPLNSCVIVSWILSPSDYKLMYFIIEWKLNED 780
 Db 721 gasvanfnltfswpmksknvqvslsaspplnsscvivswilspdyklyfielwknlned 780
 QY 781 GEIKWLRISSSVKKYYIHGKF 801
 Db 781 geikwlri:sssvkkyihdhf 801

RESULT 11

AAW50003
 ID AAW50003 standard; Protein; 896 AA.

XX AC AAW50003;

XX DT 11-JUN-1998 (first entry)

XX DE Human OB-R variant Form 3.

XX KW Detection; defective obese protein receptor; defective OB-R; human;
 XX KW defective leptin receptor; variant Form 3; infertility.

XX OS Homo sapiens.

XX PN W09741263-A1.

XX PD 06-NOV-1997.

XX PF 28-APR-1997; 97WO-US07676.

XX PR 29-APR-1996; 96US-0640389.

XX PA (PROG-) PROGENITOR INC.

XX PI Clöff J, Shafer AW, Snodgrass RH, Zupancic TJ;

XX DR WPI; 1997-549757/50.

XX DR N-PSDB; AAT95781.

XX PT Detecting defective obese protein or leptin receptor in reproductive
 XX PT cells - using variant receptor gene specific probes

XX PS Disclosure; Fig 3; 40pp; English.

XX CC The present sequence was used in the development of a novel method
 CC CC for detecting a defective obese protein or leptin receptor (OB-R)
 CC CC in cells. The method comprises contacting RNA extracted from a
 CC CC cell population (preferably an ovary, prostate, testis, sperm, ova,
 CC CC ovarian follicular or blood cell population) with an
 CC CC oligonucleotide derived from a portion of the human OB-R variant
 CC CC Form 1, 2 or 3 cDNA, and detecting hybridisation. Forms 2 and 3 are
 CC CC associated with infertility, as they are unable to correctly
 CC CC transduce signals from leptin binding. The detection method can be
 CC CC used to diagnose infertility, or predisposition to infertility,
 CC CC while treatments that inhibit or down regulate the variants, gene
 CC CC therapy to replace them in homozygotes or direct activation of
 CC CC downstream signal transduction can be used to improve fertility.
 CC CC Also described is the use of labelled DNA probes based on the OB-R
 CC CC sequence to screen for other variants.

XX SQ Sequence 896 AA;

Query Match

99.18; Score 4325; DB 18; Length 896;

Best Local Similarity 99.4%; Pred. No. 0;
 Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICORFCVLLHWEFYVITAFNLSPYTPWRFKLSCMPNPNSTYDYFLLPAGLSKNTS 60
 Db 1 micqkfcvllhweifyvitafnlspytprfkiscmpnpsdyfllpaglsknts 60
 QY 61 NGHYETAVBPKNSSGTHFSCFRSEODRNCISLCAADNTEGKTFYSTVNSLVF 120
 Db 61 ngyetavepknfsgthfscfrseodrcniscadnlegtrfystvnslvf 120
 QY 121 QOIDANNTQCNLKGDLKLFICYVESLFKNLFRNTNYKVHLLYVLPVELEDSPVPQKGS 180
 Db 121 qqidanwnlqcnlkgdlklficyveslfknlfrnynykhillyvlpveledspvpqkgs 180
 QY 181 FQMVHCNCSVHECCBCLVPVPTAKLNDLLMCKLITSGVIFQSPMSVQPINMYKPPPP 240
 Db 181 fqmvhcnscvheccclvpvptaklndllmcklitsgvgifrspmsvqpinmykpppp 240
 QY 241 LGLHMEITDDGNLKIWSWSPPLVPFPLOYQVQKYSNSTTVIREADKIVSATSLVDSILP 300
 Db 241 lglhmeitddgnlkiwswwspplvpfploqvqkysnsttvireadkivsatsllvdsilp 300
 QY 301 GSSYEVQVRGKRLDGPISWDMSTPRVFTTQDVIYFPFKILTSGVSNVSFHCYKKNKI 360
 Db 301 gssyevqvrkrlldgpgiwdmstprvfttdqvifypfkiltsvgvsnvsfhiykkenki 360
 QY 361 VPSKEIVWMLAEKIPQSDVDVSDHVSKVTFPFLNLTGKRGFTYDAVYCCNEHECHH 420
 Db 361 vpskeivwmlaeqipqsdvddvshvskvtfpflnlgtkrgfthydavyccnehechh 420
 QY 421 RYAEIYVIDVNIINISCEITDGYLTMTKCRWSTSTQSLAESTLQRLRYHSSLYCSDIPSII 480
 Db 421 ryaeliyvidvniiniscetdgyltmcrwststqslaeestlqlryhsslycsdipsii 480
 QY 481 PISEPKDCYLQSDGFYECIFQPIFLLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
 Db 481 pisepkdcylqsdgfyecifqipifllsgytmwirinhsalsgldspptcvlpdsvvklpp 540
 QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSKEVQWMEYVDKSKSVSLPV 600
 Db 541 ssvkaeitinigllkiswekvpfpennlqfiryglsgkevqwmeyvydaksksvslpv 600
 QY 601 PDLCAVAVQVRCRLDGLGYWSNWNPAFTVVMQIKVPMRGPEFWRIINGDTMKKEKNV 660
 Db 601 pdlcavavqvrckridgigyswnwnpavtvmidkvpmrspgefwrilngdtkmkeknv 660
 QY 661 TLLWKPLMKNDLSVQRYVINHTSCNGTWSVDGNGHKTFTLWTEQAHVTVLAINSI 720
 Db 661 tllwplmkndslcsqrvyvinhtscngtwsedvgnhktftlwteqahvvtvainsi 720
 QY 721 GASVANFNLTFSWPMKSNVIVQSLSAYPLNSCVIVSWILSPSDYKLMYFIIEWKLNED 780
 Db 721 gasvanfnltfswpmksknvqvslsaspplnsscvivswilspdyklyfielwknlned 780
 QY 781 GEIKWLRISSSVKKYYIHGKF 801
 Db 781 geikwlri:sssvkkyihdhf 801

RESULT 12

AAW50002
 ID AAW50002 standard; Protein; 904 AA.

XX AC AAW50002;

XX DT 11-JUN-1998 (first entry)

XX DE Human OB-R variant Form 2.

XX KW Detection; defective obese protein receptor; defective OB-R; human;
 XX KW defective leptin receptor; variant Form 2; infertility.

CC used to diagnose infertility, or predisposition to infertility,
 CC while treatments that inhibit or down regulate the variants, gene
 CC therapy to replace them in homozygotes or direct activation of
 CC downstream signal transduction can be used to improve fertility.
 CC Also described is the use of labelled DNA probes based on the OB-R
 CC sequence to screen for other variants.

XX Sequence 958 AA;

Query Match 99.1%; Score 4325; DB 18; Length 958;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIVYVTAFLNLSYPIPWFKLSKMPNSTYDYFLPAGLSKNTS 60
 Db 1 micqkfcvllhwevlyvtafnlspypwfklskmpnstydyflpagskntns 60

QY 61 NGHYETAVEPKFNSSOTHPNSLTKTTFHCCFRSEQRNCSLCAADNIEGRTFVTSNLSVF 120
 Db 61 nghyetavepkfnssgthfnslsktthccfrseqrncslcadniegrtfvtsnslvf 120

QY 121 QQIDANNITQCKLKGDLKFCVVESEFLKFLPNYKVKVHLLYVLEVEDSPLVPQKCS 180
 Db 121 qqidanwnitqcklkgdlkfcvveseflknflpnykvkvhllvyvlevedsplvpqkcs 180

QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGVIFQSPMSVQPINMVKPDP 240
 Db 181 fgmvhcnscsvheccclvpvptaklndtlmlckitsgvifrsplmsvqipnmvkpdp 240

QY 241 LGLHWEITDGNLKTSSWSPPLVPPLQVQVYSENSTTVIREADKIVSATSLLVDSILP 300
 Db 241 lglhmeitdgnlktsswspplvpplqvqvysensttvireadkivsatsllvdsilp 300

QY 301 GSSYEYQVRGKRLDGPISWDSSTPRVFTQDVIVFPKILTSVGSNVSFHCYKKNKI 360
 Db 301 gasyeyqvrgrldgpgiswdsstprvftqdvivfpkiltsvgsnvsfchcykknki 360

QY 361 VPSKEIVWMNLAEKIPQSOYDVSDHVSQVTFNNLNETKPRGFTYDAVYCCNEHECHH 420
 Db 361 vpskeivwmnlaeqipsoydvsdhvsqvtfnlnetkprgftdyavyccnehechh 420

QY 421 RYAEIYVIDVNIINISCTDGYLTMTKCRWSTSTIQSLAESTQLQYHRSSLYCSIPSIH 480
 Db 421 ryaeliyvidvniiniscetdgyltmtcrwststiqslaestqlqlyhrsslycsdpsih 480

QY 481 PISEPKDCYLOSDGFYECIFQPIFLLSGVTMIRINHSLGSLDSPCTCVLPDSVVKPLPP 540
 Db 481 pisepkdcylqsdgfyecifqpfllsgvtymirinhslgsldspctcypdsvvkplpp 540

QY 541 SSVKAEITINIGLLKISWEKPVFPENNLFQPIRYGLSGKEVQWKNYEVYDAKSQSVSLPV 600
 Db 541 ssvkaeitinigllkiswekpvfpennlfqpiiryglsgkevqwnyevydaksksvslpv 600

QY 601 PDLCAVAYQVRECKRLDGLGYSWNSNAYTVVMDIKVPMRGPEFWRIINGDTMKKERNV 660
 Db 601 pdlcavayqvreckrlldglgyswnsnaytvvmdikvpmrgpewrilingdtmkkernv 660

QY 661 TLWKPLMKNDLSQVQRVYINHHSTSCNTWSEYVGNHTKFTFLATEQARTVTVLAINSI 720
 Db 661 tlwkpmlkndlsqvrvyinhhsctwsevgntkftflateqartvtvvlainsi 720

QY 721 GASVANFNLTFSWPMKSNVQSLKSAYPLNSSCVIVSWILSPSDYKLMFYIEMKNLNE 780
 Db 721 gasvanfnltfswpmksnvqslksayplnsscvivswilspdyklnfyiemknlne 780

QY 781 GEIKWLRISSSVKKYIYHGF 801
 Db 781 geikwlrisssvkkyyihdhf 801

RESULT 14
 AAW31911

ID AAW31911 standard; Protein; 958 AA.
 XX
 AC AAW31911;
 XX
 DT 02-FEB-1998 (first entry)
 XX
 DE Human OB-R leptin receptor variant.
 XX
 KW Leptin receptor; OB-R; obese gene; obesity; gene therapy;
 diagnosis; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 85 /note= "variation from published sequence"
 FT Misc-difference 109 /note= "variation from published sequence"
 FT Misc-difference 223 /note= "variation from published sequence"
 FT Domain 845..862 /label= Transmembrane_domain
 FT Misc-difference 892..958 /note= "divergence from published sequence"
 XX
 PN W09726370-A1.
 XX
 PD 24-JUL-1997.
 XX
 PF 17-JAN-1997; 97WO-US00570.
 XX
 PR 18-JAN-1996; 96US-0508190.
 XX
 PA (PROG-) PROGENITOR INC.
 XX
 PI Clöffel J, Shafer AW, Snodgrass HR, Zupancic TJ;
 DR WPI; 1997-385353/35.
 XX N-PSDB; AAT89193.
 PT Detecting defective leptin receptor by hybridisation assay - and
 PT treatment of obesity with agent that inhibits the defective
 PT receptor, also screening for compounds that supplement leptin
 PT activity
 XX
 PS Claim 12; Fig 1A-E; 26pp; English.
 XX
 CC This polypeptide comprises a variant of the human leptin receptor
 CC (OB-R). Its sequence was deduced from a contiguous cDNA (AAT89193)
 CC derived from overlapping clones isolated from a human foetal liver
 CC library. The sequence shows near identity to a published OB-R
 CC sequence in the extracellular domain, with the exception of 3 amino
 CC acids, but there is extensive diversity in the intracellular
 CC cytoplasmic domain at the C-terminal end. A claimed method for
 CC detection of OB-R in cells comprises extraction of RNA and testing
 CC this for hybridisation to an oligonucleotide (I) derived from the
 CC OB-R variant gene, especially from the region beyond nucleotide
 CC 2770. Also claimed are methods of: (1) treating obesity by
 CC administration of an agent that inhibits expression of the OB-R
 CC variant gene; and (2) identification of a compound that can
 CC supplement activity of leptin by: (i) incubating cells expressing
 CC OB-R variant first with leptin and then with a test compound, and
 CC (ii) comparing activation signals between cells treated and not
 CC treated with the test compound. Inhibition/down-regulation of the
 CC variant OB-R (found in obese people) improves response of cells to
 CC weight regulation by leptin. Replacing variant OB-R by gene therapy
 CC (in homozygous individuals) can be used to treat obesity. Labelled
 CC probes based on the gene can be used to isolate other variant forms
 CC of the receptor gene or to detect the variant gene (e.g. for
 CC determining predisposition to obesity), while the OB-R gene can be
 CC used to express recombinant OB-R (optionally as fusion protein) and
 CC in standard hybridisation assays. The OB-R gene can also be used
 CC therapeutically in cases of overexpression of functional OB-R

CC (causing loss of appetite and hypermetabolic activity). Cells
CC engineered to express variant receptor are used in method (2) to
CC screen for (ant)agonists of leptin/ob-R interaction, also to generate
CC antibodies that competitively inhibit, neutralise or enhance activity
CC of the variant receptor.

XX Sequence 958 AA;

Query Match 99.1%; Score 4325; DB 18; Length 958;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICQKFCVLLHWEFIVYVTAFLNLSPTIPWRKLSKMPNPNSTYDFLLPAGLSKNTS 60
DB 1 micqkfcvllhwevlyvatfnlsyptipwrfklsmpnpsndydfllpaglskntns 60
QY 61 NGHYETAVEPKFNSCTHFSNLSKTTFHCCFSEQRNCSLCADNTEGKTFVSTVNSLVF 120
DB 61 nghyetavepkfnsgthfnsksatfhccfseqrncslcadnlegtfvstvnslvf 120
QY 121 QQIDANNTQCNLKGDKLFCYVESLFKFLFNRYNYKVHLLVYLVPEVLEDSPLVPQKGS 180
DB 121 qqidanwnlqcnlkgdklfcyveslflknlfrynynkvhllvlylvpevledsplvpqgs 180
QY 181 FQMVHCNCSVHECCCLVPVPTAKLNDTLMLCLKITSGGVIFQSPMLSVQPINMVKPDPP 240
DB 181 fgmvhcnscsvheccclvpvptaklndtlmlclkitsggvifrspmlsvqpinmvkpdpp 240
QY 241 LGLHMEITDGNLKIWSPPPLVPPLOQVQKYSNSTTVIREADKIVSATSLLVDSILP 300
DB 241 lglhmeitdgnlkiwsppplvpplvpploqvqkysnsttvireadkivsatsllvdsilp 300
QY 301 GSSYEVQVGRKLDGPGISDMSTPRVFTQDVIYPPPKILTSVGSNVSFHCYIKKENKI 360
DB 301 gssyevqvgkrldgpgiwdstprvftqdvlyfppkiltsvgsnvsfchcyikkenki 360
QY 361 VPSKEIVWNNLAERIPQSDYDWDHVSQVTFNNLNETKPRGKFTYDAVYCCNHECHH 420
DB 361 vpskeivwvnnlaekipqsgdydwdhvsqvtfnlnetkprgkftydavyccnechh 420
QY 421 RYAEIYVIDVNIISCTDGYLTMTKCRWSTSTIQSLAESTLQLRVHRSLSYCSIDPSTH 480
DB 421 ryaeliyvidvniisctdgyltkmcrcrststiqslaestlqlrvhrrslycsidpsih 480
QY 481 PISEPKDCYLOSGFECIFQPIELLSGYTMMIRINHSLGSLDSPPTCVLPDSVVKPLPP 540
DB 481 pisepkdcylqsgfyecifqpiellsgytmwirinhslgslsdpsptcylpdsvvkplpp 540
QY 541 SSVKAEITINIGLLKISWEKVPFPENNLQFQIRYGLSGKEVQWKYEVYDAKS SVSLPV 600
DB 541 ssvkaeitinigllklswekvpfpennlqfiryglsgkevqwkmyevydaksksvslpv 600
QY 601 PDLCAVYAVQVCKRLDGLGYNSNSNPAYTVVMDIKVPMRGPFWRIINGDTMKKEKV 660
DB 601 pdlcavayavqvrckrldggywnsnspaytvvmdikvpmrgpfrwringdtmkkekv 660
QY 661 TLLWPKLNKNDSCSVQRVIVINHHTSCNWTSEDVGNHHTKFTFLTEQAHVTVLAINSI 720
DB 661 tllwplkndscsvqrvivinhhtscngtwsedvgnhhtkftflteqahvtvvlainssi 720
QY 721 GASVANFNITFSWPMKSNVIVOSLSAYPLNSSCVISWTLSPSDYKLMYFIIEWKLNED 780
DB 721 gasvanfnitfswpmksnvivoslaysplnsscvswtllspsdyklymfiiewklned 780
QY 781 GEIKLRLISSVKKYIYHCKF 801
DB 781 geiklrlissvkkyyihdhf 801

RESULT 15

AAW19535

ID AAW19535 standard; Protein; 958 AA.

XX AAW19535;
XX 02-FEB-1998 (first entry)
XX Human OB-R leptin receptor variant.
XX Leptin receptor; OB-R; obese gene; obesity; gene therapy;
XX diagnosis; human.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Misc-difference 85 /note= "variation from published sequence"
XX Misc-difference 109 /note= "variation from published sequence"
XX Misc-difference 223 /note= "variation from published sequence"
XX Domain /note= "variation from published sequence"
XX Misc-difference 845..862 /label= Transmembrane_domain
XX Misc-difference 892..958 /note= "divergence from published sequence"
XX WO9726272-A1.
XX 24-JUL-1997.
XX 17-JAN-1997; 97WO-US00880.
XX 18-JAN-1996; 96US-0588189.
XX (PROG-) PROGENITOR INC.
XX Cioffi J, Shafer AW, Snodgrass HR, Zupancic TJ;
XX WPI: 1997-385291/35.
XX P-PSDB; AAT72649.
XX - Detecting defective form of leptin receptor by probing cellular RNA
XX - with oligonucleotide derived from DNA of receptor variant, also
XX treatment of obesity by inhibiting expression of variant receptor
XX and screening for agents that increase leptin activity
XX Claim 12; Fig 1A-E; 26pp; English.

XX This polypeptide comprises a variant of the human leptin receptor
XX (OB-R). Its sequence was deduced from a contiguous cDNA (AA72649)
XX derived from overlapping clones isolated from a human foetal liver
XX library. The sequence shows near identity to a published OB-R
XX sequence in the extracellular domain, with the exception of 3 amino
XX acids, but there is extensive diversity in the intracellular
XX cytoplasmic domain at the C-terminal end, suggesting alternative
XX splicing of a common precursor mRNA. A claimed method for
XX detection of OB-R in cells comprises extraction of RNA and testing
XX this for hybridisation to an oligonucleotide (I) derived from the
XX OB-R variant gene, especially from the region beyond nucleotide
XX 2770. Also claimed are methods of: (1) treating obesity by
XX administration of an agent that inhibits expression of the OB-R
XX variant gene; and (2) identification of a compound that can
XX supplement activity of leptin by: (i) incubating cells expressing
XX OB-R variant first with leptin and then with a test compound, and
XX (ii) comparing activation signals between cells treated and not
XX treated with the test compound. Inhibition/down-regulation of the
XX variant OB-R (found in obese people) improves response of cells to
XX weight regulation by leptin. Replacing variant OB-R by gene therapy
XX (in homozygous individuals) can be used to treat obesity. Labelled
XX probes based on the gene can be used to isolate other variant forms
XX of the receptor gene or to detect the variant gene (e.g. for
XX determining predisposition to obesity), while the OB-R gene can be
XX used to express recombinant OB-R (optionally as fusion protein) and
XX in standard hybridisation assays. The OB-R gene can also be used
XX therapeutically in cases of overexpression of functional OB-R

CC (causing loss of appetite and hypermetabolic activity). Cells
CC engineered to express variant receptor are used in method (2) to
CC screen for (ant)agonists of leptin/OB-R interaction, also to generate
CC antibodies that competitively inhibit, neutralise or enhance activity
CC of the variant receptor.
XX
XX

SQ Sequence 958 AA;

Query Match 99.1%; Score 4325; DB 18; Length 958;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 796; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MICOQKFCVLLHWEFYVITAFNLSPITPPRFKLSMPNPNSTYDFLLPAGLSKNTSNS 60
DB 1 micqkfcvllhweFYVITAFNLSPITPPRFKLSMPNPNSTYDFLLPAGLSKNTSNS 60

QY 61 NGHYETAVPEKFNSSGTHFSNLSKTFHCCEFRSEQRNCSLCAADNIEGRTFVSTVNSLVF 120
DB 61 ngHYETAVPEKfnssgthfSNLSkTFHCCEFRSEQRNCSLCAADNIEGRTFVSTVNSLVF 120

QY 121 QOIDANWNIQCHLKGDLKLFICYVESLKFNLPRNRYNYKHLLYVLPVLEDSPLVPQKGS 180
DB 121 qoidanwnIQCHlKGDLKLFICYVESLKFNLPRNRYNYKHLLYVLPVLEDSPLVPQKGS 180

QY 181 FQVHCNCSVHECCCLVPVPTAKLNDTLMLCKITSGGVIFQSPPLMSVQPINNVKPDPP 240
DB 181 fqvHCNCSvHECCCLVPVPTAKLNDTLMLCKITSGGVIFQSPPLMSVQPINNVKPDPP 240

QY 241 LGLHMEITDDGNLKITSSPPLVPFPPLQYQVYKYSNSTTVIREADKIVSATSLLVDSILP 300
DB 241 lglHMEITDDGNLKITSSPPLVPFPPLQYQVYKYSNSTTVIREADKIVSATSLLVDSILP 300

QY 301 GSSVEQVGRKRLDQPGIWSOWSTPRVFTTQDVIFPPPKILTSVGSNVSFHCIVKKNKI 360
DB 301 gssVEQVGRKRLDQPGIWSOWSTPRVFTTQDVIFPPPKILTSVGSNVSFHCIVKKNKI 360

QY 361 VPSKEIVWMNLAKIPQSOYDVSDVSHVSKVTFEFLNETKPRGKFTYDVAVCCNEHECHH 420
DB 361 vpsKEIVWMNLakIPQSOYDVSDVSHVSKVTFEFLNETKPRGKFTYDVAVCCNEHECHH 420

QY 421 RYAEIYVDVNIINISCTDGYLTMTKRWSTSTIOSLAESTLQLYHRSSLYCSDIPSIIH 480
DB 421 rYAEIYVDVniINISctdgyLTMTcrwststIOSlaestlQlyhrssLYCSDIPSIIH 480

QY 481 PISBPDCYILQSDGFYECIFQPIELLSGYTWMIRINHSLSGLSDSPPTCVLPDSVVKBLPP 540
DB 481 piSBPDCYILQSDGFYECIFQPIELLSGYTWMIRINHSLSGLSDSPPTCVLPDSVVKBLPP 540

QY 541 SSVKAEITINIGLLKISWEKVPFPENNLFQIRYGLSGKEVQWKMYEVTBAKSKSVSLPV 600
DB 541 ssvKAEITINIGLLKISWEKVPFPENNLFQIRYGLSGKEVQWKMYEVTBAKSKSVSLPV 600

QY 601 PDLCAVYAVQVRKRLDGLGYSWNSNPATVYVMDIKVPMRGPPEFNRINGDTMKKEKNV 660
DB 601 pdlCAVYAVQVRKRLDGLGYSWNSNPATVYVMDIKVPMRGPPEFNRINGDTMKKEKNV 660

QY 661 TLLWKPLMKNDLSLCSVQRYVINHHTSCNGTWSQEDVGNHTKFTFLWTEQAHTVTVLAINSI 720
DB 661 tllWKPLMKNDLSLCSVQRYVINHHTSCNGTWSQEDVGNHTKFTFLWTEQAHTVTVLAINSI 720

QY 721 GASVANFNLTFSWPMKSNIVTQSLSAVPLNNSCVIVSWILSPSDYKLMVPIEKKNLNED 780
DB 721 gasVANFNLTFSWPMKSNIVTQSLSAVPLNNSCVIVSWILSPSDYKLMVPIEKKNLNED 780

QY 781 GEIKWLRISSSVKKYYIHGKF 801
DB 781 geikwLRISssvKkYYihdhf 801

Search completed: October 22, 2001, 16:04:32
Job time: 42 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 22, 2001, 16:03:50 ; Search time 21.72 Seconds
(without alignments)
2819.721 Million cell updates/sec

Title: US-09-116-676-10

Perfect score: 4363

Sequence: 1 MICQKFCVLLHWEFIYVIT.....WLRISVVKKYIHGKETIL 804

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_68:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3355	76.9	805	2	S68441
2	3345	76.7	892	2	S68439
3	3345	76.7	894	2	S68437
4	3345	76.7	900	2	S68440
5	3345	76.7	1162	2	S68438
6	3342	76.6	1162	2	PC4184
7	3284	75.3	895	2	S74225
8	296	6.8	917	2	I49699
9	277.5	6.4	918	2	A36337
10	270.5	6.2	918	2	A44257
11	246.5	5.6	837	2	A34898
12	242.5	5.6	771	2	B38252
13	242.5	5.6	783	2	JH0329
14	242.5	5.6	863	2	C38252
15	221.5	5.1	1097	2	S17308
16	220	5.0	2302	2	T14328
17	208	4.8	1092	2	JX0312
18	178	4.1	831	2	JQ1655
19	166.5	3.8	2029	1	TDFFLK
20	165	3.8	630	2	I51086
21	163	3.7	6805	2	S20901
22	161.5	3.7	26926	1	I38344
23	157	3.6	830	2	I50455
24	157	3.6	1375	2	T13822
25	153.5	3.5	440	2	JL0144
26	153.5	3.5	460	2	JL0145
27	150.5	3.4	310	2	A29884
28	150.5	3.4	412	2	A41070
29	150.5	3.4	610	2	A36116

30 149.5 3.4 1197 2 T30581
31 149 3.4 3488 2 T34418
32 148 3.4 1000 2 I46521
33 148 3.4 1526 2 T13823
34 147.5 3.4 610 2 A34631
35 147.5 3.4 1232 2 T43027
36 146 3.3 2338 2 I73957
37 144 3.3 1825 2 T32828
38 143 3.3 638 2 A33991
39 142 3.3 1447 2 A54100
40 141 3.2 581 2 I45971
41 141 3.2 878 1 A40091
42 140.5 3.2 638 2 B28176
43 140.5 3.2 638 2 S12136
44 139 3.2 579 2 B45266
45 139 3.2 635 2 A45266

ALIGNMENTS

RESULT 1

S68441
leptin receptor, splice form Ob-Re - mouse
C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
C:Accession: S68441

R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
Nature 379, 632-635, 1996

A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
A:Reference number: S68437; MUID:96231997

A:Accession: S68441

A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA

A:Residues: 1-805 <LE>

A:Cross-references: EMBL:U49110; NID:gl195492; PIDN:AAC52424.1; PID:gl1195493

A:Experimental source: splice form Re; tissue hypothalamus

A:Note: The nucleotide sequence was submitted to the EMBL Data Library, February 1996
C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:

C:Genetics:

C:Gene: Ob-Re

C:Keywords: alternative splicing; appetite

Query Match 76.9%; Score 3355; DB 2; Length 805;
Best Local Similarity 76.0%; Pred. No. 5,3e-227;
Matches 611; Conservative 74; Mismatches 117; Indels 2; Gaps 2;

QY 1 MICQKFCVLLHWEFIYVITAFNLSPYTPMRFKLSCMPNSTYDYFLPAGLSKNTNS 60

Db 1 MICQKFCVLLHWEFIYVITAFNLSPYTPMRFKLSCMPNSTYDYFLPAGLSKNTNS 60

QY 61 NCHYETATPEPNSGTHFSNLSKTTFFHCCPRSEDRNCSLCADNIEGKTFVTSNLSVF 120

Db 61 NCHYETATPEPNSGTHFSNLSKTTFFHCCPRSEDRNCSLCADNIEGKTFVTSNLSVF 120

QY 121 QOIDANNIQCWLKGLKFLICYVSEFLKFNLRNRYKVLHLYLVLEPVEDSPVPOKGS 180

Db 121 QOIDANNIQCWLKGLKFLICYVSEFLKFNLRNRYKVLHLYLVLEPVEDSPVPOKGS 180

QY 121 ROLGVNWDIECKWKGDLFLFCHMEPLKPNFKNDKSVHLLYDLPEVIDDSPLPLKDS 180

Db 121 ROLGVNWDIECKWKGDLFLFCHMEPLKPNFKNDKSVHLLYDLPEVIDDSPLPLKDS 180

QY 181 FQVHCNCVHCECCBCLVPVFTAKLNDTLMLCKITSGVIFQSPFMSVQPIVMYKPPPP 240

Db 181 FQVHCNCVHCECCBCLVPVFTAKLNDTLMLCKITSGVIFQSPFMSVQPIVMYKPPPP 240

QY 241 LGLHMEITDDGNLKSWSPPPLVPPLQYQYKYSNSTVIREADKIVSATSLLVDSILP 300

Db 241 LGLHMEITDDGNLKSWSPPPLVPPLQYQYKYSNSTVIREADKIVSATSLLVDSILP 300

QY 301 GSSYEVQVRKRLDGPWSDMSTFRVETTDQVYFPFKILTSGVSNVSHCIYKKNKI 360

Db 301 GSSYEVQVRKRLDGPWSDMSTFRVETTDQVYFPFKILTSGVSNVSHCIYKKNKI 360

QY 299 GSSYEVQVRKRLDGPWSDMSTFRVETTDQVYFPFKILTSGVSNVSHCIYKKNKI 358

Db 299 GSSYEVQVRKRLDGPWSDMSTFRVETTDQVYFPFKILTSGVSNVSHCIYKKNKI 358

QY 361 VPSKEIVWMNLAEKIPQSDYDVSDHVSQVTFNMLNETKPRGKFTYDAVYCCNEHCCH 420

Db 361 VPSKEIVWMNLAEKIPQSDYDVSDHVSQVTFNMLNETKPRGKFTYDAVYCCNEHCCH 420

QY 361 VPSKEIVWMNLAEKIPQSDYDVSDHVSQVTFNMLNETKPRGKFTYDAVYCCNEHCCH 420

Db 361 VPSKEIVWMNLAEKIPQSDYDVSDHVSQVTFNMLNETKPRGKFTYDAVYCCNEHCCH 420

QY 361 VPSKEIVWMNLAEKIPQSDYDVSDHVSQVTFNMLNETKPRGKFTYDAVYCCNEHCCH 420

Db 361 VPSKEIVWMNLAEKIPQSDYDVSDHVSQVTFNMLNETKPRGKFTYDAVYCCNEHCCH 420

QY 361 VPSKEIVWMNLAEKIPQSDYDVSDHVSQVTFNMLNETKPRGKFTYDAVYCCNEHCCH 420

Db 361 VPSKEIVWMNLAEKIPQSDYDVSDHVSQVTFNMLNETKPRGKFTYDAVYCCNEHCCH 420

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Db 359 ISSKQIVWMRLAEKIPBQIYSIVSDRVSKVTFESNLKATRGFTYDAYCCNEQACHH 418
QY 421 RYAEYLVIVDNNINISCEFDGVLTKTCTWSTSTIOSLAESTLQLRHRSLSYCSIDIPSII 480
Db 419 RYAEYLVIVDNNINISCEFDGVLTKTCTWSTSTIOSLVGSTVQLRYHRSLSYCPDPSII 478
QY 481 PISEPKDCYLQSDGFYECIFQIFIELLSGYTWMIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
Db 479 PISEPKDCYLQSDGFYECIFQIFIELLSGYTWMIRINHSLSGSDSPPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
Db 539 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 598
QY 601 PDLCAVAVOVRCKRLDGLGYWNSWSPATLVMDIKVPMRGPEFWRIRINGDTPMKKEKNV 660
Db 599 PDLCAVAVOVRCKRLDGLGYWNSWSPATLVMDIKVPMRGPEFWRIRINGDTPMKKEKNV 658
QY 661 TLLWPKMLKNDLSQVQRYVYINHTSCNGTWSVDVGNHTKFTFLWTEQAHVTVLAINSI 720
Db 659 TLLWPKMLKNDLSQVQRYVYINHTSCNGTWSVDVGNHTKFTFLWTEQAHVTVLAINSI 718
QY 721 GASVANFNLTFSWPMKSVNIVQSLSAYPLNSCVIVSWILSPSDYKLMFYIEWKLNED 780
Db 719 GASVANFNLTFSWPMKSVNIVQSLSAYPLNSCVIVSWILSPSDYKLMFYIEWKLNED 778
QY 781 GEIKWLRISSSVKYYIHGKFTL 804
Db 779 DGMKWLRISSSVKYYIHGKFTL 802

RESULT 2
S68439
leptin receptor, splice form Ob-Rc - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
C:Accession: S68439; S68441
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; F
Nature 379, 632-635, 1996
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
A:Reference number: S68437; MUID:96231997
A:Accession: S68439
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 664-892 <LEE2>
A:Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493
A:Experimental source: splice form Rc; tissue hypothalamus
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C:Comment: For alternative splice form Re is included to produce a complete sequence
C:Genetics:
A:Gene: Ob-Rc
C:Keywords: alternative splicing; appetite

Query Match 76.7%; Score 3345; DB 2; Length 892;
Best Local Similarity 76.0%; Pred. No. 3e-226;
Matches 609; Conservative 73; Mismatches 117; Indels 2; Gaps 2;
QY 1 MICQKFCVLLHNEFYIVTAFNLSYPTIPWREKLSGMPNSTDYVFLPAGLSKNTS 60
Db 1 MNCOKFYVLLHNEFYIVTAFNLSYPTIPWREKLSGMPNSTDYVFLPAGLSKNTS 60
QY 61 NGHYETAPEKFNSSGTHSNKTTFHCCFSEQDRNCSLCADNIEGKTFVSTVNSLVF 120

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Db 61 KGASEAIVAEKFNSSGIYVPELSKTVFHCCEGQNCQNSALTDNTEGKTLASVVKASVF 120
QY 121 QQIDANNICOWKLGDLKFLFCYVESLFLKMLFRNYKVKHLLYVLPVLEDSPLVPQKGS 180
Db 121 RQGVNDWIDECWMDGJLTLFICHMEPLPKNPFKNYDKSHLLYDLPEVIDSPPLPKDS 180
QY 181 FQVHNCNSVHECECECLVPPTAKLNDTLMLCKLITSGGVIFQSPMLSVQPINVKRPDPP 240
Db 181 FQVHNCNSVHECECECLVPPTAKLNDTLMLCKLITSGGVIFQSPMLSVQPINVKRPDPP 239
QY 241 LGHMETDGNLKIWSKSPPLVPFPLOQYQVYKSENSTTVIREADKIVSATSLVDSILP 300
Db 240 LGHMETDGNLKIWSKSPPLVPFPLOQYQVYKSENSTTVIREADKIVSATSLVDSILP 298
QY 301 GSSYEYQVQVRCKRLDGLGYWNSWSPATLVMDIKVPMRGPEFWRIRINGDTPMKKEKNV 360
Db 299 GSSYEYQVQVRCKRLDGLGYWNSWSPATLVMDIKVPMRGPEFWRIRINGDTPMKKEKNV 358
QY 361 VPSKEITVMMNLAEKIPQSDYQVYSDHVSQVTFEFLNINETKPRGKFTYDAYCCNEQACHH 420
Db 359 VPSKEITVMMNLAEKIPQSDYQVYSDHVSQVTFEFLNINETKPRGKFTYDAYCCNEQACHH 418
QY 421 RYAEYLVIVDNNINISCEFDGVLTKTCTWSTSTIOSLAESTLQLRHRSLSYCSIDIPSII 480
Db 419 RYAEYLVIVDNNINISCEFDGVLTKTCTWSTSTIOSLVGSTVQLRYHRSLSYCPDPSII 478
QY 481 PISEPKDCYLQSDGFYECIFQIFIELLSGYTWMIRINHSLSGSDSPPTCVLPDSVVKPLPP 540
Db 479 PISEPKDCYLQSDGFYECIFQIFIELLSGYTWMIRINHSLSGSDSPPTCVLPDSVVKPLPP 538
QY 541 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 600
Db 539 SSVKAEITINIGLLKISWEKPVFPENNLOFQIRYGLSGKEVQWKMVEYDAKSKSVSLPV 598
QY 601 PDLCAVAVOVRCKRLDGLGYWNSWSPATLVMDIKVPMRGPEFWRIRINGDTPMKKEKNV 660
Db 599 PDLCAVAVOVRCKRLDGLGYWNSWSPATLVMDIKVPMRGPEFWRIRINGDTPMKKEKNV 658
QY 661 TLLWPKMLKNDLSQVQRYVYINHTSCNGTWSVDVGNHTKFTFLWTEQAHVTVLAINSI 720
Db 659 TLLWPKMLKNDLSQVQRYVYINHTSCNGTWSVDVGNHTKFTFLWTEQAHVTVLAINSI 718
QY 721 GASVANFNLTFSWPMKSVNIVQSLSAYPLNSCVIVSWILSPSDYKLMFYIEWKLNED 780
Db 719 GASVANFNLTFSWPMKSVNIVQSLSAYPLNSCVIVSWILSPSDYKLMFYIEWKLNED 778
QY 781 GEIKWLRISSSVKYYIHGKFTL 801
Db 779 DGMKWLRISSSVKYYIHGKFTL 799

RESULT 3
S68437
leptin receptor, splice form Ob-Ra - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
C:Accession: S68437
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.;
Nature 379, 632-635, 1996
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
A:Reference number: S68437; MUID:96231997
A:Accession: S68437
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-894 <LEE>
A:Cross-references: EMBL:U49106; NID:g1195484; PIDN:AAC52420.1; PID:g1195485
A:Experimental source: splice form Ra; tissue hypothalamus
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:
C:Genetics:
A:Gene: Ob-Ra
C:Keywords: alternative splicing; appetite

```


Query Match 76.7%; Score 3345; DB 2; Length 894;
Best Local Similarity 76.0%; Pred. No. 3.le-226;
Matches 609; Conservative 73; Mismatches 117; Indels 2; Gaps 2;

QY 1 MICQKFCVLLHWEFIYVITAFNLSTPTTPMRKFLSCMPNNTSYDYFLLPAGLSKNTSNS 60
DB 1 MMCQKFYVLLHWEFLYIAALNLAYISPWKFLFCGPPNTDDSFSLPAGAPNNASAL 60

QY 61 NGHYETAPEKFNSSGTHFNLSKTTFFHCCFRSDQNRNCSLCAONIEGKTFVTVNSLVF 120
DB 61 KGASEAIVEAKFNSSGIYVPELSKTVFHCCEGNGQNCALTONTTEGKTLASVVKASVF 120

QY 121 QOIDANNIOCLKGLDKLFICYVESLFKNLFNRYNRYKVLHLLYVLEVDSPVLVPOKGS 180
DB 121 ROLGVNWDIECMKMGDLTLFICHMEPLKPNPKFYKNDYKSVHLLYDPEVIDDSPPLPKDS 180

QY 181 FQMVHCNCSVHECCLECLVPVPTAKLNDTLMLCKLITSGGVTFQSPMLSVQPINVKPDPP 240
DB 181 FQVQCNCSLGRG-CECHVPVPRAKNLAYLLEITTSAGVSFQSPMLSLQPLVVKPDPP 239

QY 241 LGLHMEITDDGNLKSWSPPPLVPFPLOQYQVYKYSNSTTVIREADKIVSATSLLVDSILP 300
DB 241 LGLHMEITDDGNLKSWSQTMAPPFPLOQYQVYKYLENS-TIVREAAEIVSATSLLVDSVLP 298

QY 301 GSSYEVOVRKRLDGPGLIWSDMSTPRVFTTQDVYFPPKILTSVGSNVSHCIYKKNKI 360
DB 299 GSSYEVOVRKRLDGSVMSDSSPQVFTQDVYFPPKILTSVGSNASPHCIYKKNQI 358

QY 361 VPSKEIIVMMNLAEKIPQSOYDVYVSHVSKVTFNENLTKPRGFTYDVCYCCNEHCCH 420
DB 359 ISSKQIIVMMNLAEKIPQIYQVYKYLENS-TIVREAAEIVSATSLLVDSVLP 298

QY 421 RYAEIYVIVNINISCTDGLTKMTCRWSTSTIQSLAESTLQRLYHRSLSYCDIPSIIH 480
DB 419 RYAEIYVIVNINISCTDGLTKMTCRWSPSTIQSLVGVSTVQLRYHRSLSYCDIPSIIH 478

QY 481 PISEPKDCYIQSDGFEICFQPIFLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
DB 479 PTSEPKNCVLQORDGFECEVFPFLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 538

QY 541 SSVKAEITINIGLLKISWEKVPFPENNLPQIYRGLSGKEVQMKYEVYDAKSKVSLPV 600
DB 539 SNVKAETIVTGLLKISWEKVPFPENNLPQIYRGLSGKEIQWKTHEVFDKSKASLLV 598

QY 601 PDLCAVAVOVRKRLDGLGYWSNWPATVYVMDIKVPMRGPEFWRIINGDMTKKKNV 660
DB 599 SDCAVYVQVRCRRLDGLGYWSNWPATVYVMDIKVPMRGPEFWRKMDGDTVKERNV 658

QY 661 TLLWKPLMKNDLSLVQRYVINIHTSCNGTWSDEVDGHNHKTFTLWTEQAHTVTVLAINSI 720
DB 659 TLLWKPLTKNDLSLVQRYVYVVKHRTAHNGTWSDEVDGHNHKTFTLWTEQAHTVTVLAINSL 718

QY 721 GASVANFNLTFSMPKSVKNTVQSLAYPLNSCVIVSWILSPDYKLMYPIIEMKNLNEED 780
DB 719 GASLVNFNLTFSMPKSVKSAVESLSAYPLSSCVILSWTLPDDYSLLYLVIEWKILNEED 778

QY 781 GEIKWLRISSSVKYYTHGKF 801
DB 779 DGMKWLRIPSNVKKEFIHDFN 799

RESULT 4
S68440
leptin receptor, splice form Ob-Rd - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Dec-2000
C:Accession: S68440
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; et al.
Nature 379, 632-635, 1996
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
A:Reference number: S68437; MUID:96231997
A:Accession: S68440

A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-900 <LEE>
A:Cross-references: EMBL:U49109; NID:g1195490; PIDN:AAC52423.1; PID:g1195491
A:Experimental source: tissue hypothalamus
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:
C:Genetics:
A:Gene: Ob-Rd
C:Keywords: alternative splicing; appetite; transmembrane protein
F:840-860/Domain: transmembrane #status predicted <TM>

Query Match 76.7%; Score 3345; DB 2; Length 900;
Best Local Similarity 76.0%; Pred. No. 3.le-226;
Matches 609; Conservative 73; Mismatches 117; Indels 2; Gaps 2;

QY 1 MICQKFCVLLHWEFIYVITAFNLSTPTTPMRKFLSCMPNNTSYDYFLLPAGLSKNTSNS 60
DB 1 MMCQKFYVLLHWEFLYIAALNLAYISPWKFLFCGPPNTDDSFSLPAGAPNNASAL 60

QY 61 NGHYETAPEKFNSSGTHFNLSKTTFFHCCFRSDQNRNCSLCAONIEGKTFVTVNSLVF 120
DB 61 KGASEAIVEAKFNSSGIYVPELSKTVFHCCEGNGQNCALTONTTEGKTLASVVKASVF 120

QY 121 QOIDANNIOCLKGLDKLFICYVESLFKNLFNRYNRYKVLHLLYVLEVDSPVLVPOKGS 180
DB 121 ROLGVNWDIECMKMGDLTLFICHMEPLKPNPKFYKNDYKSVHLLYDPEVIDDSPPLPKDS 180

QY 181 FQMVHCNCSVHECCLECLVPVPTAKLNDTLMLCKLITSGGVTFQSPMLSVQPINVKPDPP 240
DB 181 FQVQCNCSLGRG-CECHVPVPRAKNLAYLLEITTSAGVSFQSPMLSLQPLVVKPDPP 239

QY 241 LGLHMEITDDGNLKSWSPPPLVPFPLOQYQVYKYSNSTTVIREADKIVSATSLLVDSILP 300
DB 241 LGLHMEITDDGNLKSWSQTMAPPFPLOQYQVYKYLENS-TIVREAAEIVSATSLLVDSVLP 298

QY 301 GSSYEVOVRKRLDGPGLIWSDMSTPRVFTTQDVYFPPKILTSVGSNVSHCIYKKNKI 360
DB 299 GSSYEVOVRKRLDGSVMSDSSPQVFTQDVYFPPKILTSVGSNASPHCIYKKNQI 358

QY 361 VPSKEIIVMMNLAEKIPQSOYDVYVSHVSKVTFNENLTKPRGFTYDVCYCCNEHCCH 420
DB 359 ISSKQIIVMMNLAEKIPQIYQVYKYLENS-TIVREAAEIVSATSLLVDSVLP 298

QY 421 RYAEIYVIVNINISCTDGLTKMTCRWSTSTIQSLAESTLQRLYHRSLSYCDIPSIIH 480
DB 419 RYAEIYVIVNINISCTDGLTKMTCRWSPSTIQSLVGVSTVQLRYHRSLSYCDIPSIIH 478

QY 481 PISEPKDCYIQSDGFEICFQPIFLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 540
DB 479 PTSEPKNCVLQORDGFECEVFPFLSGYTMWIRINHSLSGLSDSPPTCVLPDSVVKPLPP 538

QY 541 SSVKAEITINIGLLKISWEKVPFPENNLPQIYRGLSGKEVQMKYEVYDAKSKVSLPV 600
DB 539 SNVKAETIVTGLLKISWEKVPFPENNLPQIYRGLSGKEIQWKTHEVFDKSKASLLV 598

QY 601 PDLCAVAVOVRKRLDGLGYWSNWPATVYVMDIKVPMRGPEFWRIINGDMTKKKNV 660
DB 599 SDCAVYVQVRCRRLDGLGYWSNWPATVYVMDIKVPMRGPEFWRKMDGDTVKERNV 658

QY 661 TLLWKPLMKNDLSLVQRYVINIHTSCNGTWSDEVDGHNHKTFTLWTEQAHTVTVLAINSI 720
DB 659 TLLWKPLTKNDLSLVQRYVYVVKHRTAHNGTWSDEVDGHNHKTFTLWTEQAHTVTVLAINSL 718

QY 721 GASVANFNLTFSMPKSVKNTVQSLAYPLNSCVIVSWILSPDYKLMYPIIEMKNLNEED 780
DB 719 GASLVNFNLTFSMPKSVKSAVESLSAYPLSSCVILSWTLPDDYSLLYLVIEWKILNEED 778

QY 781 GEIKWLRISSSVKYYTHGKF 801
DB 779 DGMKWLRIPSNVKKEFIHDFN 799

```

RESULT 5
S68438
leptin receptor, splice form Ob-Rb - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1998 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
C:Accession: S68438; S68441
R:Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, J.G.; Lee, J.I.; et al
Nature 379, 632-635, 1996
A:Title: Abnormal splicing of the leptin receptor in diabetic mice.
A:Reference number: S68437; MUID:96231937
A:Accession: S68438
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 664-1162 <LEE1>
A:Cross-references: EMBL:U49107; NID:g1195486; PIDN:AAC52424.1; PID:g1195487
A:Experimental source: splice form Rb; tissue hypothalamus
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
A:Note: only a part of the translation is shown
A:Accession: S68441
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-796, GNCVLPMD' <LEE2>
A:Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493
A:Experimental source: splice form Re; tissue hypothalamus
A:Note: this nucleotide sequence was submitted to the EMBL Data Library, February 1996
A:Note: this sequence from splice form Re is included to produce a complete sequence
C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S68440
C:Genetics:
A:Gene: Ob-Rb
C:Keywords: alternative splicing; appetite

Query Match 76.7%; Score 3345; DB 2; Length 1162;
Best Local Similarity 76.0%; Pred. No. 4.4e-226;
Matches 609; Conservative 73; Mismatches 117; Indels 2; Gaps 2;

QY 1 MICQKFCVLLHWEFIVITAFNLSTYPTPPFKLSCMPNPTDYELLPAGLSKNTS 60
Db 1 MICQKFCVLLHWEFIVITAFNLSTYPTPPFKLSCMPNPTDYELLPAGLSKNTS 60
QY 61 NGHYETAVEPKNSGTHFNSLSKTTFFCCFSEQDRNCSLCAADIEGKTFVSTVNSLVF 120
Db 61 KGASEAIVEAKFNSSGIYVPELSKTVFHCCEGQEQNSALTONTEGKTLASVVKASVF 120
QY 121 QOIDANNIOCKLKGDLKIFICYVESLEKFLFRNYNKVHLLYVLPEVLEDSPLVPQKGS 180
Db 121 ROLGVNWDIECMKGDLTFLICHMEPLKPNPKNYDSKVHLLYDLPEVIDDSPLPLKDS 180
QY 181 FQVHCNCSVHECCBCLVPVPTAKLNDTLMLCKLITSGGVIFQSPLMVSWQPINVVKPDPP 240
Db 181 FQVHCNCSLRC-CECHVPVPRKLNLYALLYLEITSAGVSFQSPMLSLQPLMVLVVKPDPP 239
QY 241 LGLHMEITDDGNLKTSSGSPPLVPPFQYQVYKYSNSTTVIREADKIVSATSLLDVSLP 300
Db 240 LGLHMEITDDGNLKTSSGSPPLVPPFQYQVYKYSNSTTVIREADKIVSATSLLDVSLP 298
QY 301 GSSVEVQVRGRKLDGPGTWSQSPRPVFTTQDYVFPFKILTSGVSNVSPHICVYKKNKI 360
Db 301 GSSVEVQVRGRKLDGPGTWSQSPRPVFTTQDYVFPFKILTSGVSNVSPHICVYKKNKI 360
QY 361 VPSKEIVWMNLAKIPQSDVYVSDRVSKVTFEENLNKTRPKRGFTVDVAVCCNEHCCH 420
Db 361 VPSKEIVWMNLAKIPQSDVYVSDRVSKVTFEENLNKTRPKRGFTVDVAVCCNEHCCH 420
QY 421 RYAEYVIDVNIINISCTDGYLTWTCTWSTSTQSLAESTLQRYHRSLSYCDIPSIIH 480
Db 421 RYAEYVIDVNIINISCTDGYLTWTCTWSTSTQSLAESTLQRYHRSLSYCDIPSIIH 480
QY 481 PISPKDCYQSDGFCICFQIPILLSGYTWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
Db 481 PISPKDCYQSDGFCICFQIPILLSGYTWIRINHSGLSDSPPTCVLPDSVVKPLPP 540
QY 479 PTSEPKNCVLQDQGFYECVQPIFLLSGYTWIRINHSGLSDSPPTCVLPDSVVKPLPP 538
Db 479 PTSEPKNCVLQDQGFYECVQPIFLLSGYTWIRINHSGLSDSPPTCVLPDSVVKPLPP 538

QY 541 SSVKAETITNIGLKISWEKPPENNLOFOIRYGLSGKEVQWKMVEYVDKSKSVLPV 600
Db 539 SNVKAETITNIGLKISWEKPPENNLOFOIRYGLSGKEVQWKMVEYVDKSKSVLPV 598
QY 601 PDCAVAVOVRCRLDGLGYGWSNPNPAYTVVYMDIKVPMRGPEFWRIINGDTPMKKEKNV 660
Db 599 SDLCAYVYVQVRCRLDGLGYGWSNPNPAYTVVYMDIKVPMRGPEFWRIINGDTPMKKEKNV 658
QY 661 TLWKKPLMKNDSCSVORYVINHTSCNGTSEDVGNHNTKFTFLWTEQAHVTYVLAINSI 720
Db 659 TLWKKPLMKNDSCSVORYVINHTSCNGTSEDVGNHNTKFTFLWTEQAHVTYVLAINSI 718
QY 721 GASVANFNLTFSWPMKSNVIVQSLAYSAYPLNSCVIVSWILSPSDYKLMYFIEMKKNLNE 780
Db 719 GASVANFNLTFSWPMKSNVIVQSLAYSAYPLNSCVIVSWILSPSDYKLMYFIEMKKNLNE 778
QY 781 GEIKWLRISSVKKYIHKGF 801
Db 779 DGMKWLRISSVKKYIHKGF 799

RESULT 6
PC4184
leptin receptor, Ob-Rb - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 01-Dec-2000
A:Accession: JC4895; JC4896; JC4897; PC4184; JC4797
R:Takaya, K.; Ogawa, Y.; Isse, N.; Okazaki, T.; Satoh, N.; Masuzaki, H.; Mori, K.; et al
Biochem. Biophys. Res. Commun. 225, 75-83, 1996
A:Title: Molecular cloning of rat leptin receptor isoform complementary DNAs-identifi
A:Reference number: JC4895; MUID:96332408
A:Accession: JC4895
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1162 <TAK>
A:Cross-references: DDBJ:D85558; NID:g1526441; PIDN:BAAL2831.1; PID:d1013515; PID:g15
A:Accession: JC4896
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-889, 'RADTL' <TA2>
A:Cross-references: DDBJ:D85557
A:Accession: JC4897
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-796, 'G', 1157-1158, 'TVLLN' <TA3>
A:Cross-references: DDBJ:D85559
R:Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.
Biochem. Biophys. Res. Commun. 224, 597-604, 1996
A:Title: Substitution at codon 269 (glutamine-proline) of the leptin receptor (OB-R)
A:Reference number: PC4184; MUID:96295531
A:Accession: PC4184
A:Molecule type: mRNA
A:Residues: 840-1162 <IID>
A:Cross-references: DDBJ:D84550
R:Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, K.
Biochem. Biophys. Res. Commun. 222, 19-26, 1996
A:Title: Phenotype-linked amino acid alteration in leptin receptor cDNA from Zucker f
A:Reference number: JC4797; MUID:96212906
A:Accession: JC4797
A:Molecule type: mRNA
A:Residues: 1-889, 'RADTL' <IID>
A:Cross-references: DDBJ:D84125; NID:g1374707; PIDN:BAAL2230.1; PID:g1374708
A:Experimental source: adipose cell
C:Comment: This receptor is obese-phenotype-linked mutant, found in the Zucker (fa/fa)
C:Genetics:
A:Gene: fa
C:Keywords: appetite; transmembrane protein
F:840-860/Domain: transmembrane #status predicted <TMM>
F:861-1162/Domain: intracellular #status predicted <INT>

Query Match 76.6%; Score 3342; DB 2; Length 1162;
Best Local Similarity 76.0%; Pred. No. 7.1e-226;

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Matches 609; Conservative 74; Mismatches 116; Indels 2; Gaps 2;

QY 1 MTCQKFCVLLHWEFYVITAFNLSPYTPWRFKLSMCPNPNSTYDFLLPAGLSKNTS 60
 Db 1 MTCQKFCVLLHWEFYVITAFNLSPYTPWRFKLSMCPNPNSTYDFLLPAGLSKNTS 60
 QY 61 NGHETAVPEKNSGTHFNSLKTTHCCFSEQRNCSLACADNIEGKTFVSTVNSL 120
 Db 61 KGASEALVEAKFNSTGIYVSELSKTFIFCCFCNEQONCSALTGNTGKTLASVVKPLVF 120
 QY 121 QQIDANWNIQCKLGLKLFICYVESLFKNLFRNYKYVHLLYVLPVEVLEDSPLVPKGS 180
 Db 121 ROLGVNWDIECHMKGDLTLFICHMEPLLNPKFNKYDSKVHLLYDLPVLDLPLPKDS 180
 QY 181 FQVHCNCSVECECCCLVPVPTAKLNDTLMLCKITSGGVIFQSPILMSVQPINMYKPPDP 240
 Db 181 FQVHCNCSVRE-CECHVPVPRAKVNYALLMYLEITSAGVSFQSPILMSVQPINMYKPPDP 239
 QY 241 LGLHMEITDDGNLKTISWSSPPLVPFPLOQVYKSNSTVIREADKIVSATSLLVDSILP 300
 Db 241 LGLHMEITDDGNLKTISWSSPPLVPFPLOQVYKSNSTVIREADKIVSATSLLVDSILP 300
 QY 299 GSSYEVOVRSKRLDGSVWDSLSLQFLTQDVYFPFKILTSGVSNASFCIYKNEQT 358
 Db 299 GSSYEVOVRSKRLDGSVWDSLSLQFLTQDVYFPFKILTSGVSNASFCIYKNEQT 358
 QY 361 VPSKEIVWMNLAEKIPQSDVSDHVSQVTFNKLNETKPRGKFTYDAVYCCNEHCCH 420
 Db 361 VPSKEIVWMNLAEKIPQSDVSDHVSQVTFNKLNETKPRGKFTYDAVYCCNEHCCH 420
 QY 421 RYAEIYVDVNIINISCTDGYLTMTKCRWSTIQSLAESTLQRLYHRSLSYCDIPSIH 480
 Db 421 RYAEIYVDVNIINISCTDGYLTMTKCRWSTIQSLAESTLQRLYHRSLSYCDIPSIH 480
 QY 481 PISEPKCYLQSDGYECIFQIFLLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLPP 540
 Db 481 PISEPKCYLQSDGYECIFQIFLLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLPP 540
 QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSKEVQWKMYEYDAKSASLPV 600
 Db 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSKEVQWKMYEYDAKSASLPV 600
 QY 599 SDLCAYVAVQVRCRLDGLGYWNSNPAYTVMDIKVPMRGPEFWRINGDTHKKEKNV 660
 Db 599 SDLCAYVAVQVRCRLDGLGYWNSNPAYTVMDIKVPMRGPEFWRINGDTHKKEKNV 660
 QY 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLWTEQAHVTVLAINSI 720
 Db 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLWTEQAHVTVLAINSI 720
 QY 721 GASVANFNLTFSWPMKSNVIVQSLSAYPLNSCVIVSWILSPSDYKLYFIEMKNLND 780
 Db 721 GASVANFNLTFSWPMKSNVIVQSLSAYPLNSCVIVSWILSPSDYKLYFIEMKNLND 780
 QY 781 GEIKWLRISSSVKYYIHGKF 801
 Db 781 GEIKWLRISSSVKYYIHGKF 801
 QY 779 DGMKWLRISSSVKYYIHGKF 799
 Db 779 DGMKWLRISSSVKYYIHGKF 799

RESULT 7

S74225

leptin receptor, isoform Ob-Rf - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 05-Nov-1999

C:Accession: S74225

R:Wang, M.Y.; Zhou, Y.T.; Newgard, C.B.; Unger, R.H.

FEBS Lett. 392, 87-90, 1996

A:Title: A novel leptin receptor isoform in rat.

A:Reference number: S74225; MUID:96368027

A:Accession: S74225

A:Molecule type: mRNA

A:Residues: 1-895 <WAN>

A:Cross-references: EMBL:U53144; NID:g1395212; PIDN:AAB03088.1; PID:g1395213

A:Experimental source: strain Sprague-Dawley; tissue type brain
 C:Genetics:
 A:Gene: rOb-R
 C:Keywords: appetite; transmembrane protein
 F:840-860/Domain: transmembrane #status predicted <TM>

Query Match 75.3%; Score 3284; DB 2; Length 895;
 Best Local Similarity 75.0%; Pred. No. 5.7e-222;
 Matches 601; Conservative 77; Mismatches 121; Indels 2; Gaps 2;

QY 1 MTCQKFCVLLHWEFYVITAFNLSPYTPWRFKLSMCPNPNSTYDFLLPAGLSKNTS 60
 Db 1 MTCQKFCVLLHWEFYVITAFNLSPYTPWRFKLSMCPNPNSTYDFLLPAGLSKNTS 60
 QY 61 NGHETAVPEKNSGTHFNSLKTTHCCFSEQRNCSLACADNIEGKTFVSTVNSL 120
 Db 61 KGASEALVEAKFNSTGIYVSELSKTFIFCCFCNEQONCSALTGNTGKTLASVVKPLVF 120
 QY 121 QQIDANWNIQCKLGLKLFICYVESLFKNLFRNYKYVHLLYVLPVEVLEDSPLVPKGS 180
 Db 121 ROLGVNWDIECHMKGDLTLFICHMEPLLNPKFNKYDSKVHLLYDLPVLDLPLPKDS 180
 QY 181 FQVHCNCSVECECCCLVPVPTAKLNDTLMLCKITSGGVIFQSPILMSVQPINMYKPPDP 240
 Db 181 FQVHCNCSVRE-CECHVPVPRAKVNYALLMYLEITSAGVSFQSPILMSVQPINMYKPPDP 239
 QY 241 LGLHMEITDDGNLKTISWSSPPLVPFPLOQVYKSNSTVIREADKIVSATSLLVDSILP 300
 Db 241 LGLHMEITDDGNLKTISWSSPPLVPFPLOQVYKSNSTVIREADKIVSATSLLVDSILP 300
 QY 299 GSSYEVOVRSKRLDGSVWDSLSLQFLTQDVYFPFKILTSGVSNASFCIYKNEQT 358
 Db 299 GSSYEVOVRSKRLDGSVWDSLSLQFLTQDVYFPFKILTSGVSNASFCIYKNEQT 358
 QY 361 VPSKEIVWMNLAEKIPQSDVSDHVSQVTFNKLNETKPRGKFTYDAVYCCNEHCCH 420
 Db 361 VPSKEIVWMNLAEKIPQSDVSDHVSQVTFNKLNETKPRGKFTYDAVYCCNEHCCH 420
 QY 421 RYAEIYVDVNIINISCTDGYLTMTKCRWSTIQSLAESTLQRLYHRSLSYCDIPSIH 480
 Db 421 RYAEIYVDVNIINISCTDGYLTMTKCRWSTIQSLAESTLQRLYHRSLSYCDIPSIH 480
 QY 481 PISEPKCYLQSDGYECIFQIFLLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLPP 540
 Db 481 PISEPKCYLQSDGYECIFQIFLLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLPP 540
 QY 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSKEVQWKMYEYDAKSASLPV 600
 Db 541 SSVKAEITINIGLLKISWEKVPFPENNLOFQIRYGLSKEVQWKMYEYDAKSASLPV 600
 QY 599 SDLCAYVAVQVRCRLDGLGYWNSNPAYTVMDIKVPMRGPEFWRINGDTHKKEKNV 660
 Db 599 SDLCAYVAVQVRCRLDGLGYWNSNPAYTVMDIKVPMRGPEFWRINGDTHKKEKNV 660
 QY 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLWTEQAHVTVLAINSI 720
 Db 661 TLLMKPLMKNDLSLCSVQRYVINHHTSCNGTWSDEVGNHTKFTFLWTEQAHVTVLAINSI 720
 QY 721 GASVANFNLTFSWPMKSNVIVQSLSAYPLNSCVIVSWILSPSDYKLYFIEMKNLND 780
 Db 721 GASVANFNLTFSWPMKSNVIVQSLSAYPLNSCVIVSWILSPSDYKLYFIEMKNLND 780
 QY 781 GEIKWLRISSSVKYYIHGKF 801
 Db 781 GEIKWLRISSSVKYYIHGKF 801
 QY 779 DGMKWLRISSSVKYYIHGKF 799
 Db 779 DGMKWLRISSSVKYYIHGKF 799

RESULT 8

I49699

glycoprotein 130 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Jul-2000

C:Accession: I49699; I48370
R:Saito, M.; Yoshida, K.; Hibl, M.; Taga, T.; Kishimoto, T.
J. Immunol. 148, 4066-4071, 1992
A:Title: Molecular cloning of a murine IL-6 receptor-associated signal transducer, gp130
A:Reference number: I48370; MUID:92291532
A:Accession: I49699
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>
A:Cross-references: GB:M83336; NID:9193591; PIDN:AAA37723.1; PID:9193592
A:Accession: I48370
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-917 <RES>
A:Cross-references: EMBL:X62646; NID:9840816; PIDN:CAA44515.1; PID:9840817
C:Genetics: gp130
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein
F:134-314/Domain: cytokine receptor homology <CRS>

Query Match 6.8%; Score 296; DB 2; Length 917;
Best Local Similarity 22.8%; Pred. No. 9.5e-13;
Matches 121; Conservative 95; Mismatches 214; Indels 100; Gaps 26;

QY 323 STPRVFTTQDIYE-----PPKILTSVGSNVSFHCYKK---ENKIVP 362
DB 2 SAPRIWLAQLFFLTTESIGOLLEPCGYIPEFVVGQSGNFTALCVLKEACLAQHYYVN 61

QY 363 SKEIYVMNLAEKIPQSDVYVSDHVKVTFNLTNPKRGFTYDAVYCCNEHECHRY 422
DB 62 ASYIVKTNHA-AVPREQVTVNRTTSSVTFDVA-VLPVOL-----CNILSFGQIE 112

QY 423 RELYVI-----DVNINISC-ETDGYLTKMTCRWSTSTIOSLAESTIQLRYHRSLLYC 473
DB 113 QNVYGVTLGSPFPDPKPTNLTCIVNEG--KNMLCQWDPG-----RETLETNYTLKSEWA 165

QY 474 SDIPSIIPISEPKCYLQSDGFYECI---FQPIFLSGYTMIRINHSGLSDSPPTCVLP 531
DB 166 TE-----KPPDC--QSKHGTSQVMYTPYYVN-IEVWVEAENALGKVSSEINFD 214

QY 532 DSVVKPLPSSVKAEITINI-GLLKISKEKVPENNLOFOIRYGLSG-----KQVQ--- 582
DB 215 VDKVKPTPYNLSTNSELSSILKLSW-----VSSGIGLLDLKSDIQRT 261

QY 583 -----WKMEYVDKAKSVSLPVPDL--CAVYAVQVRCRLDGLGYSNWSNPAYTVYMD 635
DB 262 KDASTWIOVPLEDTMSPTSTFTVODLKPFTEYVFRIRSIKDGKGYSDWSEASGTTYE 321

QY 636 IKVPMRGPEFWRILNGDPMKEKNVTLWPKMNDLSCSVQRY--VINHHITSCNGTWSE 693
DB 322 DR-PSRPPSPFYKTNPSHGQYRSVRLIWKALPLSEANGKILDYEIVLTQSKVSQYTV 380

QY 694 DVGHTKFTFLWTEQAHVTIVLAINSIGASVANENLFSWP-MSKVNIVQSLAYPLNS 752
DB 381 ---TGELTVNLNDRYVAVSLAARKVKGSAAV-LTIPSPHTVAAYSVNKKAPP-KDN 435

QY 753 CVIYSWILSPSDYKLMFYIIEKWNLEDGEI--KWLRISSSVKYYIHGK 800
DB 436 LLWVEW--TPPKPKVYILEWCVLSENAPCVEDQWQEDATVNTHLRGR 483

RESULT 9
membrane glycoprotein gp130 precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 28-Jul-2000
C:Accession: A36337
R:Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A:Title: Molecular cloning and expression of an IL-6 signal transducer, gp130.
A:Reference number: A36337; MUID:9108484

A:Accession: A36337
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-918 <HIB>
A:Cross-references: GB:M57230; NID:9186353; PIDN:AAA59155.1; PID:9186354
C:Genetics: gp130
A:Gene: GDB:IL6ST; GPI30
A:Cross-references: GDB:126725; OMIM:600694
A:Map position: 5q11-5q11
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; membrane protein
F:134-316/Domain: cytokine receptor homology <CRS>

Query Match 6.4%; Score 271.5; DB 2; Length 918;
Best Local Similarity 22.7%; Pred. No. 1.9e-11;
Matches 112; Conservative 82; Mismatches 227; Indels 73; Gaps 22;

QY 337 PPKILTSVGSNVSFHCYKK---ENKIVPSKEIVVMNLAEKIPQSDVYVSDHVKVTF 393
DB 33 PESPVQLHSNFTAVCVLKEKCMDFHVNANTYVNTN-HFTIPKEQVTVINRTASSVTF 91

QY 394 FNLNETKPRGFTYDAVYCCNEHECHRYAELVYIDV-----NINISC-ETDGYLTK 444
DB 92 TDI-----ASLNIQTCNLTFTGQLEQNVYITIIISGLPPEKPKNLSCIVNEG--KK 141

QY 445 MTCRWSTSTIOSLAESTIQLRYHRSLLYCSIDPSIHPISPEKDCYLOSDGFYECI--FOP 502
DB 142 MRCWDGG-----RETHLETNFTLKESEAT-----HKFA---DCKAKRDTPTSCVTVDYST 188

QY 503 IFLSGYTMIRINHSGLSDSPPTCVLPDSVVKPLPSSVKAEITINI-----IGLLKISW 558
DB 189 VYFVN-IEVWVEAENALGKVTSDHINFDPVYKVKPNPPHNL-----VINSEELSLTLKLTW 244

QY 559 EKP-----VFPENNLOFOIRYGLSKKEVQWKMVEYVDKAKSVSLPVPDL--CAVYAVOV 611
DB 245 TNPISKSVIILKYNIOYRTKDAST-----WSQIPEDPASTRSSTFTVODLKPFTEYVERI 299

QY 612 RCKRLDGLGYSNWSNPAYTVYMDIKVPMRGPEFWRILNGDPMKEKNVTLWPKMKN 671
DB 300 RCMKEDCKGYSDWSEASGITYEDR-PSKAPSFYWKIDPSHTOGYRTVQLVWLTLPPE 358

QY 672 SLCSVQRYKVINHHITSCNGTWSEVGNH-----TKFTFLWTEQAHVTIVLAINSIGASVANF 727
DB 359 ANGKILDYEV-----LTRWKSHLQNTVNTKLTNLTNDRYLATLTVRLVKGSDAAV 413

QY 728 NLTFSPWPKSVNIQSLAYSAYPLNSCVISVILSPSDYKLMFYIIEKWNLEDGE--IKW 785
DB 414 LTIPACDFQATHPYMDLKAFP-KDNMLWVETTPRESVK--KYILEWCVLSDKAPCIITDW 470

QY 786 LRISSSVKYYIHG 799
DB 471 QOEDGTVHRTYLRG 484

RESULT 10
A44257
interleukin-6 signal transducing molecule gp130 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 28-Jul-2000
C:Accession: A44257
R:Wang, Y.; Nesbitt, J.E.; Fuentes, N.L.; Fuller, G.M.
Genomics 14, 666-672, 1992
A:Title: Molecular cloning and characterization of the rat liver IL-6 signal transducer
A:Reference number: A44257; MUID:93052397
A:Accession: A44257
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-918 <WAN>
A:Experimental source: liver
A:Note: sequence extracted from NCBI backbone (NCBI:118488)
C:Superfamily: cytokine receptor homology
C:Keywords: transmembrane protein

394 FNLNETKPGKFYY-----DAVCCNEHECHRYAELVYDVININISCTDGYITKMTC 447
 ||| | | : | |
91 PHNYQ----AFUFLCPWEDSVOLLQDELHAGYPPA-----SPSNLSCLMHLTNSLVC 143
 ||| | | : | |

DD 244 PQAGCLQLCWE-PWQGLHINOKCELRHKPQGEASWALV6-----PLPLEALQ 291

QY 602 -DLCAV-----YAVQVCKRLDGLGYWSNWSNPAYTVVMDIKVPMRGP-----EFWRIN 650

Db 292 YELGILLPATATYLTQIRCMPLPGHSDWS-PS-----LELRTTERTAPTVRDLTWR--- 343
QY 651 GDTMKKEKNVTLLMKNDLSLCVQRYVNHHTS-----CNGTWSVDGNHTKF 701
Db 344 -OROLDPRTVLFKPKVPLEDSGRIOGYVWRPSPGAGAILPLCNTT-----ELSC 395
QY 702 TFLWTEQAHVTTLAINSIGASVANFNLTFSWPKSKVNIQSLAYSPLNNSCVIVSWILS 761
Db 396 TFHLPSEAQVALVAYNSAGTSRPT-PWVES--ESRGPALTRLHAMARDPHSLWVGW--E 450
QY 762 PSDYKLMYFIIEW 774
Db 451 PPNWPQGYVIEW 463
RESULT 13
JH0329
granulocyte colony-stimulating factor receptor D7 precursor - human
C:Species: Homo sapiens (man)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-Nov-1999
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.; Son
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor: a
A:Reference number: JH0329; MUID:91079757
A:Accession: JH0329
A:Molecule type: mRNA
A:Residues: 1-783 <LAR>
A:Cross-references: GB:M55720; NID:g31698; PIDN:CAA39252.1; PID:g31699
A:Experimental source: placenta
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-783/Product: granulocyte colony-stimulating factor receptor D7 #status predicted <F>
F:25-627/Domain: extracellular #status predicted <EXT>
F:628-653/Domain: transmembrane #status predicted <TRA>
F:654-783/Domain: intracellular #status predicted <INT>
F:93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 5.6%; Score 242.5; DB 2; Length 783;
Best Local Similarity 22.7%; Pred. No. 4.3e-09;
Matches 112; Conservative 75; Mismatches 183; Indels 123; Gaps 25;
QY 341 LTSVGSNVSFRCIYKKE-NKIVPSKEIYVMMNLAEKIPQSQYDVVSD--HVSQVTFEFLN 397
Db 35 IVHLGDPITASSIIKQNGSHLDPEQILRLG-AEQLPGGRQRLSDGTQESITPLHLN 93
QY 398 ETKPRGKFTYDAVYCCNEHCHRYAEIYVID-----VNINISCTDGYLTGMT 446
Db 94 HTQ-----AFLSG-----CLNMGNSLIQILDQVELRAGYPPAIPHNLSCJLMLNLTSSLI 141
QY 447 CRWSTSTIQSLAES-TLQRYHRSLLYCSIDIPSHPISEPKDCYLOSDGFECI----- 499
Db 142 QWEPGPETHLPTSTLKSFRSG-----NCTQGDSDILDCVPKDGQS 184
QY 500 -----FQPIFLSSGYTWIRNHSLGSDSPPTCVLPDVSVKPLPP-----SSVRAEIT 548
Db 185 HCCIPRKHLLYQNGMIWQAEALGTSMSPOLCLDPMVVKLEPPMLRMTWDPSPA-AP 243
QY 549 INIGLLKISWEKVPFP-ENNLQFOIRYGLSGREVQKMYEVDAKSKSVSLPVP----- 601
Db 244 PQAGCLQLCHE-PWQGLHINQKELRHKFORGEASWALVG-----PLPLEALQ 291
QY 602 -DLCAV-----YAVQVCKRLDGLGYSWNSNPAYTVVMDIKVPMRCP-----EFWRILN 650
Db 292 YELGILLPATATYLTQIRCMPLPGHSDWS-PS-----LELRTTERTAPTVRDLTWR--- 343
QY 651 GDTMKKEKNVTLLMKNDLSLCVQRYVNHHTS-----CNGTWSVDGNHTKF 701
Db 344 -OROLDPRTVLFKPKVPLEDSGRIOGYVWRPSPGAGAILPLCNTT-----ELSC 395
QY 702 TFLWTEQAHVTTLAINSIGASVANFNLTFSWPKSKVNIQSLAYSPLNNSCVIVSWILS 761
Db 396 TFHLPSEAQVALVAYNSAGTSRPT-PWVES--ESRGPALTRLHAMARDPHSLWVGW--E 450
QY 762 PSDYKLMYFIIEW 774
Db 451 PPNWPQGYVIEW 463

Db 396 TFHLPSEAQVALVAYNSAGTSRPT-PWVES--ESRGPALTRLHAMARDPHSLWVGW--E 450
QY 762 PSDYKLMYFIIEW 774
Db 451 PPNWPQGYVIEW 463
RESULT 14
C38252
granulocyte colony-stimulating factor receptor precursor, long form - human
N:Contains: granulocyte colony-stimulating factor, long form; granulocyte colony-stim
C:Species: Homo sapiens (man)
C>Date: 14-Jun-1991 #sequence_revision 30-Jan-1993 #text_change 05-Nov-1999
C:Accession: C38252; JH0330; A46486; S68332; S21607
R:Fukunaga, R.; Seto, Y.; Mizushima, S.; Nagata, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 8702-8706, 1990
A:Title: Three different mRNAs encoding human granulocyte colony-stimulating factor r
A:Reference number: A38252; MUID:91062348
A:Accession: C38252
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-863 <FUK>
A:Cross-references: GB:M59820; GB:M38027; NID:g183048; PIDN:AAA63178.1; PID:g183049
A:Note: Clones pHG11 and pHG5
A:Accession: A38252
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-680,708-863 <FU2>
A:Cross-references: GB:M59818; GB:M38025; NID:g183046; PIDN:AAA63176.1; PID:g183047
A:Note: clone pHQ3
R:Larsen, A.; Davis, T.; Curtis, B.M.; Gimpel, S.; Sims, J.E.; Cosman, D.; Park, L.;
J. Exp. Med. 172, 1559-1570, 1990
A:Title: Expression cloning of a human granulocyte colony-stimulating factor receptor
A:Reference number: JH0329; MUID:91079757
A:Accession: JH0330
A:Molecule type: mRNA
A:Residues: 1-680,708-863 <LAR>
A:Cross-references: GB:X5721; NID:g31696; PIDN:CAA39253.1; PID:g31697
A:Note: clone 25-1; placenta
R:Seto, Y.; Fukunaga, R.; Nagata, S.
J. Immunol. 148, 259-266, 1992
A:Title: Chromosomal gene organization of the human granulocyte colony-stimulating fa
A:Reference number: A46486; MUID:92091782
A:Accession: A46486
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 855-863 <SET>
A:Cross-references: GB:S71484; NID:g240883; PIDN:AAB20660.1; PID:g240884
A:Experimental source: granulocyte
A:Note: sequence extracted from NCBI backbone (NCBIN:71484, NCBI:P:71485)
R:Haniu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.
Arch. Biochem. Biophys. 324, 344-356, 1995
A:Title: Extracellular domain of granulocyte-colony stimulating factor receptor.
A:Reference number: S68331; MUID:96132662
A:Accession: S68332
A:Molecule type: protein
A:Residues: 234-269 <HAN>
C:Genetics:
A:Gene: GDB:CSF3R
A:Cross-references: GDB:126430; OMIM:138971
A:Map position: lp35-lp34.3
C:Keywords: alternative splicing; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-863/Product: granulocyte colony-stimulating factor receptor, long form #status p
F:25-680,708-863/Product: granulocyte colony-stimulating factor receptor, short form
F:25-627/Domain: extracellular #status predicted <EXT>
F:628-653/Domain: transmembrane #status predicted <TRA>
F:654-863/Domain: intracellular #status predicted <INT>
F:93,128,134,389,474,579,610/Binding site: carbohydrate (Asn) (covalent) #status pred
Query Match 5.6%; Score 242.5; DB 2; Length 863;
Best Local Similarity 22.7%; Pred. No. 4.9e-09;

Matches 112; Conservative 75; Mismatches 183; Indels 123; Gaps 25;

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QY 341 LTSVGSNVSFFCIYKKE--NKIVSPKEIYVWNNLAERKIPQSDYDVSD--HYSKVTFEFLN 397
Db 35 IVHGDPTASCIIKQNCSHLDPEQIILWRIG-AELQPGGRQRLSDGTQBSIITPLHN 93
QY 398 ETKPRGFTYDAVYCCNEHCHRYAEIYVID-----VNINISCTDGYLTGMT 446
Db 94 HTQ-----AFLSC-----CLNWCNSLIQILDQVELRAGYPPAIPHNLSCLMNTTSLI 141
QY 447 CRWSTSTTQSLAES--TLQRYHRSSLYCSDIPSHPISEPKDCYLQSDGFYECI----- 499
Db 142 QWEPGPEPETHLPTFTLKSRSG-----NCOTQGSILDCVPKDGQS 184
QY 500 -----FOPIELLSGYTWIRINHSLDSDPTCVLPDSVVKPLPP-----SSVKAEIT 548
Db 185 HCCIPRKHLLYQNGIWAQENALGTSMPQLCDPMDVVKLEPPMLRMTDPSPEA-AP 243
QY 549 INIGLLKISWEKVPFP--ENNLOPIRYGLSGKEVQWKMVEYDAKSKSVSLPVP----- 601
Db 244 PQAGCLQCNW-PHQPLGHINQKELRHKKPQGEASWALVG-----PLPLEALQ 291
QY 602 -DLCAV-----YAVQVRCKRLDGLGYNSNPNAYTVVMDIKVPMRGP-----EFWRIN 650
Db 292 YELGCLLPATAYTLQIRCPWPLGHWSDWS-PS-----LELRTTERAPTVRLDTWWR--- 343
QY 651 GDTWKKEKNTLLWKLPMKNDLSLVQRYVINHHTS-----CNCWSEDVGNHTKF 701
Db 344 -ORLDPRTVOLFKPVPLEDSGRIGYVVSWRPQAGAILPLCNT-----ELSC 395
QY 702 TFLTEQAHTVTVLAINSIGASVANFNLTSPWMSKVNIVQSLISAYPLNSCIVSWILS 761
Db 396 TFLPSEAEVALVAYNSAGTSRPT-PWFS--ESRGPALTRLHARDPHSLWGW--E 450
QY 762 PSDYKLMYFIEW 774
Db 451 PNPWPQGYVIEW 463

RESULT 15
S17308
leukemia inhibitory factor receptor - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999
C:Accession: S17308
R:Geating, D.P.; Thut, C.J.; VandenBos, T.; Gimpel, S.D.; Delaney, P.B.; King, J.; Price
EMBO J. 10, 2839-2848, 1991
A:Title: Leukemia inhibitory factor receptor is structurally related to the IL-6 signal
A:Reference number: S17308; MUID:92007727
A:Accession: S17308
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1097 <GEA>
A:Cross-references: GB:X61615; NID:g34365; PIDN:CAA43805.1; PID:g34366

Query Match 5.1%; Score 221.5; DB 2; Length 1097;
Best Local Similarity 20.0%; Pred. No. 2e-07;
Matches 143; Conservative 127; Mismatches 292; Indels 153; Gaps 33;

QY 161 LLVVLPEVLEDSPLVPKQSGFQMVHC-----NCS-----VHECC----- 194
Db 35 LLYLMQVNSQ-----KKGAPHDLKCVTNLQVWNCWKAPSGTGRCTDYEVCIENRSR 89
QY 195 -----ECLVPVPTAKLNDTLMLCKITSGGVIFQSPILMSVQPINNVKPPDPLGLHMEIT- 248
Db 90 CYOLEKTSIKIPALSHGDEYITINSLHDFGSSTSKFTLNEQVSLI-PDTPETILNSADF 148
QY 249 DDGNLKSWSPPPLVPPQYQVYKYSNSTTVIR-----EADKIVSATPSLL----- 294
Db 149 STSTLYLKNWDRGSV-FPHRSNVIW-----EIKVLKESMELVKLVTHNTLNGKDTLHWS 204
QY 295 --VDSILPGSSYEVQVR-----GKRLDGPGLWSDNSPTPRVT---TQDYIYFPFKILTSVG 345
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Db 205 WASDPLECAHFVEIRCYIDNLHFSGLEWSDWSPVKNISWIPDSQTKVFPQDKVILVG 264
QY 346 SNVSHGCIYKKEKIVPSPKEIYVWNNLAERKIPQSDYDVSD--SDHVKVTFEFLNETKPR 402
Db 265 SDITFCV-----SQEKV-----LSALIGHTNCPILHLDGENVA-IKIRNISVSASS 310
QY 403 GKFTYDAVYCCNEHCHRYAEIYVIDVNINISCTDGYLTGMTCRWSTSTQSLA---E 459
Db 311 GT---NVFTTEDNIFGTIVIFAGYPPDTPQOLNCEHD-LKEIICSWNPGRVTAIVGPA 366
QY 460 STLQRLYHRSSLYCSDIPSHPISEPKDCYLQSDGFYECIYFQPIELLSGYTWIRINHSL 519
Db 367 TSYTLVESFGKYVRLKRAEPTNES-----YOLLFQMLPNOEIYNTLNAHNP 416
QY 520 GSDSPPTCVLPDSVVKPLPPSSVKAEITINIGLLKISWEKP-----VFPEP 566
Db 417 GRSQSTILVNITEKVY-PHTPTSEKVK-DINSTAVKLSWHLPGNFKINFCEIEIKSN 474
QY 567 NLQPIRYGLSGKEVQWKMVEYDAKSKSVSLPVPDLCAVYAVQVRCKRLDGLGYNSWS 626
Db 475 SVQBRNVTIKGVE-----NSSYLVALDKLNPTLYTFRIGS-TETFWKWSKS 523
QY 627 NPATVVMYDIKVPMRGPEFWRIINGDTMKKEKNVTLLWKLPMKNDLSLVQRYVINHHTS 686
Db 524 NKKOHLTTEAS-PSKGGPTWREWSSD-----GKNLIYTKPLPINEA-----NGKILSTNVS 574
QY 687 CNG-----TWSEDVGNHTKFTFLWTEQAHTVTVLAINSIGASVANFNLTSPWMSKVNIV 741
Db 575 CSSDEETQSLSEIPDPQHKAEIRLDKNDYIISVAKNSVSGSSPSKIASMEIPNDLKE 634
QY 742 QSLISAYPLNSCIVSWILSPS---DYKLMYFIEWKN--LNEDGEIKWLRISSS 791
Db 635 QVYGM-----GKGILLTWHYDPNMTCDY-----VIKMCNSRSEPCCLMDWRKVPSPN 680
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Search completed: October 22, 2001, 16:04:59
Job time: 69 sec
